

# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 10-29-02  
Searcher: Beverly e 4994  
Terminal time: 20  
Elapsed time: 0  
CPU time: \_\_\_\_\_  
Total time: 23  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

### Search Site

\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S

### Type of Search

\_\_\_\_ N.A. Sequence  
\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_ IG Suite  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
\_\_\_\_ Other CGN

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09-MAR-2000; 2000US-0188064.  
PR  
13-MAR-2000; 2000US-0188880.  
PR  
03-APR-2000; 2000US-0194344.  
PR  
23-JUN-2000; 2000US-0213861.  
PR  
11-JUL-2000; 2000US-0217369.  
PR  
11-JUL-2000; 2000US-0217370.  
PR  
14-JUL-2000; 2000US-0218337.  
PR  
20-JUL-2000; 2000US-0218492.  
XX  
XX  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
XX  
PI  
Vogeli G, Wood LS, Parodi LA, Lind P;  
XX WPI: 2001-570628/64.  
DR  
N-PSDB: AAS42857.  
DR  
XX  
PT New isolated nucleic acid encoding a new G-protein coupled receptor  
PT polypeptide for detecting receptor modulators that can treat mental  
PT disorders, such as schizophrenia, anxiety, depression, or obesity -  
XX  
XX

Claim 35; Page 90; 279pp; English.

CC Sequences AAU25554, AAU25616 represent human G-protein coupled receptor  
CC (GPCR) polypeptides of the invention. The proteins and their associated  
CC DNA sequences can be used to identify compounds which bind to GPCR  
CC polypeptides and in screening for compounds that modulate GPCR activity.  
CC By screening a human subject for the presence of mutations in GPCR DNA, a  
CC GPCR-related disorder or a genetic predisposition can be diagnosed. The  
CC sequences can also be used for treatment and prevention of mental  
CC disorders such as schizophrenia, attention deficit disorder, anxiety,  
CC depression, dementia and bipolar disorder, neurological disorders such as  
CC Huntington's disease, Parkinson's disease and Tourette's syndrome,  
CC metabolic disorders such as obesity, anorexia and type 2 diabetes,  
CC cardiovascular disorders such as thrombosis, myocardial infarction,  
CC cardiomyopathy and atherosclerosis, viral infections caused by HIV and  
CC cancers.

S0	Sequence	508 AA;
	Query Match	99.9%; Score 2641; DB 22; Length 508;
	Best Local Similarity	Pred. No. 6.5e-234;
Matches	507; Conservative	1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTSCTNSTRRSNSHHCMPJLSPKMPISLAHIIITSTVLVFLAASFGNIVLALVLORK	60
Db	1	MTSCTNSTRRSNSHHCMPJLSPKMPISLAHIIITSTVLVFLAASFGNIVLALVLORK	60
Qy	61	QLLOQVTRNFIFNLVTDLLQISLVAWPVVAISVPLFPLWNSHFCETALVSLTHLFAFASVN	1200
Db	61	QLLOQVTRNFIFNLVTDLLQISLVAWPVVAISVPLFPLWNSHFCETALVSLTHLFAFASVN	1200
Qy	121	TTIVASVDRYLSTIIHPLSPSKMTQRRGYLLLTGTWIVAILQSTPPLVYGMOAFAFERNA	1800
Db	121	TTIVASVDRYLSTIIHPLSPSKMTQRRGYLLLTGTWIVAILQSTPPLVYGMOAFAFERNA	1800
Qy	181	LCSMTMGASPSYITLISVSVFIVPLIYMIACYSVFPCFCAARRQHALYVNRKHSLEVYVKD	2400
Db	181	LCSMTMGASPSYITLISVSVFIVPLIYMIACYSVFPCFCAARRQHALYVNRKHSLEVYVKD	2400
Qy	241	CVENENDEGCAKKEEFODESEFFRRQHOGEYVAKEGMBADKGSJLAKEGSCTGSESSVEA	3000
Db	241	CVENENDEGCAKKEEFODESEFFRRQHOGEYVAKEGMBADKGSJLAKEGSCTGSESSVEA	3000
Qy	301	RGSEEVRESSTVASDGSMECKEGSTKYAENSMKADKGRTEVNCQSIDLGEDDMFEGEDDI	3600
Db	301	RGSEEVRESSTVASDGSMECKEGSTKYAENSMKADKGRTEVNCQSIDLGEDDMFEGEDDI	3600
Qy	361	NFSEDDVEAVNIPBSLPSRRSNSNPPLPRCYOCKAKAVYFIITISYVSLSGPYCLAV	4200
Db	361	NFSEDDVEAVNIPBSLPSRRSNSNPPLPRCYOCKAKAVYFIITISYVSLSGPYCLAV	4200
Qy	421	LAVWVDETQYPPQWVITIIIMLFLOCCIHRYVYGYMHKTIKKETQMLKKPFCKEPRK	4800
Db	421	LAVWVDETQYPPQWVITIIIMLFLOCCIHRYVYGYMHKTIKKETQMLKKPFCKEPRK	4800

Db 421 LAAVAVDVEYQPVWVITIIIMLFELLOCCIIHPHYGVYGMHKTIKKEIQMLAKFKCEKRPK 480

QY 481 EDSHDPDLPTGEGTGEGKIVPSYDATTTP 508  
|||||  
481 EDSHDPDLPTGEGTGEGKIVPSYDATTTP 508

Db 481 EDSHDPDLPTGEGTGEGKIVPSYDATTTP 508

RESULT 2  
AAB86428  
ID AAB86428 standard; Protein; 508 AA

AC AAB86428;

DT 19-OCT-2001 (first entry)

Human brain SERALPHA protein.

KW SERALPHA; human; brain; G protein receptor; medicine.

OS Homo sapiens.

PN DE10004930-A1.

PD 09-AUG-2001.

PF 04-FEB-2000; 2000DE-1004930.

PR 04-FEB-2000; 2000DE-1004930.

PA (BRUE/) BRUESS M.  
PA (BOEN/) BOENTSCH H

XX	Bruno M Boonisch H.
PT	

XX  
DB WPT: 2001-1000007/54

DR N-PSDB; AAH48673.  
YY

PT Gene encoding a protein of the G protein receptor super family, having homology to neurotransmitter receptors is useful to develop new

PT medicaments -  
XX

PS Disclosure; Page 4; 8pp; German  
XX

CC This invention describes a novel human brain-derived G protein receptor  
CC and its encoding protein designated SFRALPHA. The recanor or cells

CC expressing the receptor are used to develop new medicines, chemicals and technologies, and to devalue existing medicines and technologies.

XX	Sequence	508 AA
50		

Query Match	99.9%	Score 2641	DB 22	Length 508
Best Local Similarity	99.8%	Pred. No. 6.5e-234		
Matches 507; Conservative	1;	Mismatches 0	Indels 0	Gaps 0;

QY	1	MTSTCSTNRSSNSHTCMPLSKMPISLAHHIIINSTVLVFLAASFNGNIVLVLORCP	60
Db	1	MTSTCSTNRSSNSHTCMPLSKMPISLAHHIIINSTVLVFLAASFNGNIVLVLORCP	60
QY	61	OLLOVNTNFFIENLVTDLLOISLVAWVAVTSVBLEFMPLNSHFCTALVSLTHLEAFASVN	1200
Db	61	OLLOVNTNFFIENLVTDLLOISLVAWVAVTSVBLEFMPLNSHFCTALVSLTHLEAFASVN	1200
QY	121	TIIVAVSVDRYRSTIIHPILSPSKMQRKGYLLVGTWIVALLQSPRLVYMGGOAAFDERNA	1800
Db	121	TIIVAVSVDRYRSTIIHPILSPSKMQRKGYLLVGTWIVALLQSPRLVYMGGOAAFDERNA	1800
QY	181	LCSMIWGASPSYTLISVVSFVILVLIWIAIACYSVVFCARROHALLVYNRHSLSEVVKD	2400
Db	181	LCSMIWGASPSYTLISVVSFVILVLIWIAIACYSVVFCARROHALLVYNRHSLSEVVKD	2400
QY	241	CVENDEDEGACRKEPFODESEFRQROHEBEVYNAKAGRMELANDSILAKAEGSTGSESSVEA	3000
Db	241	CVENDEDEGACRKEPFODESEFRQROHEBEVYNAKAGRMELANDSILAKAEGSTGSESSVEA	3000

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QY 301 RGSEEVRESSTVASDGSMEKKEGSKTEKVENSMKADKRTTEVNOCSIDLGEDDMEFGDDI 360
DB 301 RGSEEVRESSTVASDGSMEKKEGSKTEKVENSMKADKRTTEVNOCSIDLGEDDMEFGDDI 360
QY 361 NFSEDDVEAVNIPESLPPSRNSNSNPDLPRCYOCKAKAVIIFIISYVLSLGPYCLAV 420
DB 361 NFSEDDVEAVNIPESLPPSRNSNSNPDLPRCYOCKAKAVIIFIISYVLSLGPYCLAV 420
QY 421 LAVWVDETVQPMVITIIIMLFLOCCIHPIYVGYGMHKTIKKEIDMLKFFCKEKRPK 480
DB 421 LAVWVDETVQPMVITIIIMLFLOCCIHPIYVGYGMHKTIKKEIDMLKFFCKEKRPK 480
QY 481 EDSDHPDLPGTEGTEGTEKIVPSYDSATRP 508
DB 481 EDSDHPDLPGTEGTEGTEKIVPSYDSATRP 508

RESULT 3
AAU04369
ID AAU04369 standard; Protein; 508 AA.
XX
AC AAU04369;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human G-protein coupled receptor, hRUP15.
XX
KW Human; G-protein coupled receptor; GPCR; hRUP15; agonist;
XX
OS Homo sapiens.
XX
PN MO200136471-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000MO-US31509.
XX
PR 17-NOV-1999; 99US-0166088.
XX
PR 17-NOV-1999; 99US-0166099.
XX
PR 17-NOV-1999; 99US-0166369.
XX
PR 23-DEC-1999; 99US-0171900.
XX
PR 23-DEC-1999; 99US-0171901.
XX
PR 23-DEC-1999; 99US-0171902.
XX
PR 11-FEB-2000; 2000US-0181749.
XX
PR 14-MAR-2000; 2000US-0189258.
XX
PR 14-MAR-2000; 2000US-0189259.
XX
PR 10-APR-2000; 2000US-0195898.
XX
PR 10-APR-2000; 2000US-0195899.
XX
PR 10-APR-2000; 2000US-0196078.
XX
PR 28-APR-2000; 2000US-0200419.
XX
PR 12-MAY-2000; 2000US-0203630.
XX
PR 12-JUN-2000; 2000US-0210741.
XX
PR 12-JUN-2000; 2000US-0210982.
XX
PR 21-AUG-2000; 2000US-0226760.
XX
PR 26-SEP-2000; 2000US-0235418.
XX
PR 26-SEP-2000; 2000US-0235779.
XX
PR 20-OCT-2000; 2000US-0242332.
XX
PR 20-OCT-2000; 2000US-0242343.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Lowitz KP.
XX
DR MPI: 2001-355616/37.
XX
DR N-PSDB; AAS07942.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents -
XX
XX Claim 29; Page 102-104; 160pp; English.

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XX
CC The sequence represents a human G-protein coupled receptor (GPCR),
CC hRUP15. The endogenous and non-endogenous, constitutively activated
CC versions of human G-protein coupled receptors (GPCR), are useful for
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer.
CC Non-endogenous version of human GPCRs are also utilized in research
CC settings and in vitro and in vivo system, incorporating GPCRs can be
CC utilized to elucidate and understand the roles these receptors
CC play in the human condition, both normal and diseased.
XX
QY Sequence 508 AA:
DB
QY Query Match 99.9%; Score 2641; DB 22; Length 508;
DB Best Local Similarity 99.8%; Pred. No. 6,5e-234;
DB Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTSTCTNSTRESNSHRCMPLSKPIISLAGIIRSYLVIFLAASFVGNIVLVLQRP 60
DB 1 MTSTCTNSTRESNSHRCMPLSKPIISLAGIIRSYLVIFLAASFVGNIVLVLQRP 60
QY 61 QLLQVTRFIENLVTDLQISLVAPWVATSVPLFPLNSHFCALVSLTLFAFASVN 120
DB 61 QLLQVTRFIENLVTDLQISLVAPWVATSVPLFPLNSHFCALVSLTLHLFAFASVN 120
QY 121 TIYVSVDRILSTIHPISTYSKMTQRRGYLLYGTWVAILLOSTPPLYGNGQAAFDERRA 180
DB 121 TIYVSVDRILSTIHPISTYSKMTQRRGYLLYGTWVAILLOSTPPLYGNGQAAFDERRA 180
QY 181 LCSMIMGASPSYITLSVVSFVIPIYIMACYSVFCAAROHALLNVNRHSLEAVKD 240
DB 181 LCSMIMGASPSYITLSVVSFVIPIYIMACYSVFCAAROHALLNVNRHSLEAVKD 240
QY 241 CVENEDEGAKEKEEFODESEFRROHEGEVYAKEGREAKDGLAKEGSTGTSSESVEA 300
DB 241 CVENEDEGAKEKEEFODESEFRROHEGEVYAKEGREAKDGLAKEGSTGTSSESVEA 300
QY 301 RGSEEVRESSTVASDGSMEKKEGSKTEKVENSMKADKRTTEVNOCSIDLGEDDMEFGDDI 360
DB 301 RGSEEVRESSTVASDGSMEKKEGSKTEKVENSMKADKRTTEVNOCSIDLGEDDMEFGDDI 360
QY 361 NFSEDDVEAVNIPESLPPSRNSNSNPDLPRCYOCKAKAVIIFIISYVLSLGPYCLAV 420
DB 361 NFSEDDVEAVNIPESLPPSRNSNSNPDLPRCYOCKAKAVIIFIISYVLSLGPYCLAV 420
QY 421 LAVWVDETVQPMVITIIIMLFLOCCIHPIYVGYGMHKTIKKEIDMLKFFCKEKRPK 480
DB 421 LAVWVDETVQPMVITIIIMLFLOCCIHPIYVGYGMHKTIKKEIDMLKFFCKEKRPK 480
QY 481 EDSDHPDLPGTEGTEGTEKIVPSYDSATRP 508
DB 481 EDSDHPDLPGTEGTEGTEKIVPSYDSATRP 508

RESULT 4
AAG64126
ID AAG64126 standard; Protein; 508 AA.
XX
AC AAG64126;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human G-protein-coupled receptor GPRV72.
XX
KW Human; guanosine triphosphate binding protein-coupled receptor;
KW G-protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;
KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;
KW Alzheimer's disease; cytostatic; hepatocytic; neurotropic;
KW neuroprotective; gene therapy; peptide therapy.
XX
XX Homo sapiens.
XX

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	XX	MO200148188-A1.	
	PD	05-JUL-2001.	
XX	PF	28-DEC-2000; 2000WO-JP09408.	
XX	PR	28-DEC-1599; 99JP-0375152.	
XX	PR	31-MAR-2000; 2000JP-0101339.	
XX	PA	(HELI-) HELIX RES INST.	
XX	XI	Matsumoto S, Oda T, Salto Y, Morikawa N, Yoshida K, Suwa M;	
PI	P1	Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;	
CC	DR	WPI: 2001-425662/45.	
CC	N-PSDB:	AAM73517.	
PT	PT	New DNA encoding guanosine triphosphate binding protein coupled receptors and their expression products for screening potential anticancer and nootropic drugs and in diagnosis of these diseases - Claim 1; Page 135-138; 170pp; Japanese.	
CC	XX	The invention relates to nine human guanosine triphosphate binding protein (G protein)-coupled receptors designated GPRV8, GPRV16, GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the genes encoding them. These genes and proteins and antibodies against the protein are useful in the treatment, prevention, diagnosis and investigation of diseases associated with G protein-coupled receptors, including cancer, cirrhosis of the liver and Alzheimer's disease. The present sequence is a G protein-coupled receptor of the invention.	
CC	XX	Sequence 508 AA:	
QQ	Query Match	99.9%; Score 2641; DB 22; Length 508; Best local similarity 99.8%; Pred. No. 6,5e+234;	
	Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
OY	I	MTSTCTNSTRESNSSHTCMPLSKMPDISLHAGIIIRSTVLVIFFLAASFVNIVLVLYLRKP 60	
DQ	1	MTSTCTNSTRESNSSHTCMPLSKMPDISLHAGIIIRSTVLVIFFLAASFVNIVLVLYLRKP 60	
OY	61	QLLOVTNRFIFLAVTDLLTSLVPWWVVATSPLEFPLNSHFCAALVSFLHPAFASYN 120	
DQ	61	QLLOVTNRFIFLAVTDLLTSLVPWWVVATSPLEFPLNSHFCAALVSFLHPAFASYN 120	
OY	121	TIVVSVVDRLSIILHPLSYPSKMRTORGYLLYGTMVAIALOSTPEPLYGWGOADEFERNA 180	
DQ	121	TIVVSVVDRLSIILHPLSYPSKMRTORGYLLYGTMVAIALOSTPEPLYGWGOADEFERNA 180	
OY	181	LCSMWGASPSFTILISVSFYIPILVMIAACSVVFCAARRRHALLNNKRSLERYAKD 240	
DQ	181	LCSMWGASPSFTILISVSFYIPILVMIAACSVVFCAARRRHALLNNKRSLERYAKD 240	
OY	241	CVENENDEGAEEKKEFEODESEFRROHBEERVAKKEGRMEAKDOSLKAEGSTTSSESSYA 300	
DQ	241	CVENENDEGAEEKKEFEODESEFRROHBEERVAKKEGRMEAKDOSLKAEGSTTSSESSYA 300	
OY	301	RGSSEVERESTVASDSMGEKGSTKVEENSMAKADKRTENVOCSIDJGEDMERGEDDI 360	
DQ	301	RGSSEVERESTVASDSMGEKGSTKVEENSMAKADKRTENVOCSIDJGEDMERGEDDI 360	
OY	361	NFSEDDVAVNPESLPSPRRSNSNPNPLPCRYOCKRAKVITIIIIFSYYLSLGPPCFCLAV 420	
DQ	361	NFSEDDVAVNPESLPSPRRSNSNPNPLPCRYOCKRAKVITIIIIFSYYLSLGPPCFCLAV 420	
OY	421	LAVWDVETOVPOWVITTIIMLFEOCCIHPRVUYUMHNTIKTEIODMLKKFPCEKPKR 480	
DQ	421	LAVWDVETOVPOWVITTIIMLFEOCCIHPRVUYUMHNTIKTEIODMLKKFPCEKPKR 480	
OY	481	EDSHFDLPGBTGEGTKIVPSTDATFP 508	
DQ	481	EDSHFDLPGBTGEGTKIVPSTDATFP 508	

RESULT 5  
AAU04387  
ID AAU04387 Standard; Protein; 926 AA.  
AC AAU04387;  
XX  
DT 23-OCT-2001 (first entry)  
XX  
DE GPCR-Gs fusion protein, hRUP15-GS.  
XX  
KW G-protein coupled receptor; GPCR; hRUP15-Gs; agonist;  
XX Inverse agonist; Lung cancer.  
OS Chimeric - Homo sapiens.  
OS Chimeric - Rattus sp.  
XX  
PN W0200136471-A2.  
XX  
PD 25-MAY-2001.  
XX  
PE 16-NOV-2000; 2000MO-USJ1509.  
XX  
FR 17-NOV-1999; 99US-0166088.  
FR 17-NOV-1999; 99US-0166099.  
FR 17-NOV-1999; 99US-0166369.  
PR 23-DEC-1999; 99US-0171900.  
PR 23-DEC-1999; 99US-0171901.  
PR 23-DEC-1999; 99US-0171902.  
PR 11-FEB-2000; 2000US-0181749.  
PR 14-MAR-2000; 2000US-0189258.  
PR 14-MAR-2000; 2000US-0189259.  
PR 10-APR-2000; 2000US-0195898.  
PR 10-APR-2000; 2000US-0195899.  
PR 10-APR-2000; 2000US-0196078.  
PR 28-APR-2000; 2000US-0200419.  
PR 12-MAY-2000; 2000US-0203630.  
FR 12-JUN-2000; 2000US-0210781.  
FR 12-JUN-2000; 2000US-0210982.  
PR 21-AUG-2000; 2000US-0226760.  
PR 26-SEP-2000; 2000US-0235418.  
PR 26-SEP-2000; 2000US-0235779.  
PR 20-OCT-2000; 2000US-0242332.  
PR 20-OCT-2000; 2000US-0242343.  
XX  
PA (AREN-) ARENA PHARM INC.  
XX  
PI Chen R, Dang HT, Lowitz KP;  
XX  
DR WPI: 2001-355616/37.  
DR N-PSDB; AAS08274.  
XX  
PT Endogenous and non-endogenous versions of human G-protein coupled  
XX receptors for direct identification of candidate compounds as agonists  
XX inverse agonists or partial agonists for use as therapeutic agents -  
XX  
XX Example 5; Page 151-154; 160pp; English.  
XX  
XX The sequence is a G-protein coupled receptor (GPCR) fusion protein,  
CC hRUP15-Gs, being the human hRUP15 fused to the rat Gs protein.  
CC The endogenous and non-endogenous, constitutively activated versions  
CC of human G-protein coupled receptors (GPCR), are useful for direct  
CC identification of candidate compounds as receptor agonists, inverse  
CC agonists or partial agonists having applicability as therapeutic  
CC agents for treating diseases related to GPCR, e.g. lung cancer.  
CC Non-endogenous version of human GPCRs are also utilized in research  
CC settings and in vitro and in vivo system, incorporating GPCRs can be  
CC utilised to elucidate and understand the roles these receptors  
CC play in the human condition, both normal and diseased.  
XX  
XX Sequence 926 AA;

Query Match 99.9%; Score 2641; DB 22; Length 926;  
 Best Local Similarity 99.8%; Pred. No. 1.5e-233;  
 Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60  
 DB 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60  
 QY 61 QLLQVTRNFIFNLVLTDLQISLVAAPVAVTSVPLFPLNSHFTALVSLTHLFAFASVN 120  
 DB 61 QLLQVTRNFIFNLVLTDLQISLVAAPVAVTSVPLFPLNSHFTALVSLTHLFAFASVN 120  
 QY 121 TIVLVSDRYLSTIHPILSPYSKMTQRRGYLLTGWTVAIIQSTPPLXGMOAFAFDRNA 180  
 DB 121 TIVLVSDRYLSTIHPILSPYSKMTQRRGYLLTGWTVAIIQSTPPLXGMOAFAFDRNA 180  
 QY 181 LCSMIMGASPSYTLISVSVFIVPLIYMIACYSVFCARROHALLVNRKHSLEVRKD 240  
 DB 181 LCSMIMGASPSYTLISVSVFIVPLIYMIACYSVFCARROHALLVNRKHSLEVRKD 240  
 QY 241 CVENEDDEGAKEKEEFODESEFRQHGHEVYKAKGRMEAKDGLAKEGSTGTSSEVYA 300  
 DB 241 CVENEDDEGAKEKEEFODESEFRQHGHEVYKAKGRMEAKDGLAKEGSTGTSSEVYA 300  
 QY 301 RGSEEVRESSSTVASDGSMEGKEGSTKYEENSMKADKGRTEVNOCSIDLGEDDMFEGDDI 360  
 DB 301 RGSEEVRESSSTVASDGSMEGKEGSTKYEENSMKADKGRTEVNOCSIDLGEDDMFEGDDI 360  
 QY 361 NFSEDDEAVANIPESLPPSRNSNSNPPLRCYCCKAKAVIFIIIFSVYLSLGPYCFLAY 420  
 DB 361 NFSEDDEAVANIPESLPPSRNSNSNPPLRCYCCKAKAVIFIIIFSVYLSLGPYCFLAY 420  
 QY 421 LAAWVDEVETQVQWVITIIILFLLQCCIHPIYVGYMHTIKKEIDMLKKFCKEKP 480  
 DB 421 LAAWVDEVETQVQWVITIIILFLLQCCIHPIYVGYMHTIKKEIDMLKKFCKEKP 480  
 QY 481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508  
 DB 481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508

RESULT 6  
 AAB61982  
 ID AAB61982 standard; protein: 508 AA.  
 AC AAB61982;  
 XX 14-MAY-2001 (first entry)  
 DE Human G-protein coupled receptor, IGSL.  
 KW G-protein coupled receptor; IGSL; psychiatric; central nervous system;  
 movement disorder; tremor; Tourette's syndrome; Parkinson's disease;  
 Huntington's disease; dyskinesia; dystonia; spasm; neuroleptic; human;  
 neotropic; anticonvulsant; relaxant; vaccine; gene therapy.  
 OS Homo sapiens.  
 XX WO200109184-A1.  
 PN 08-FEB-2001.  
 PD 17-JUL-2000; 2000WO-EP06878.  
 PF 15-JUL-1999; 99EP-0202326.  
 PR 15-JUL-1999; 99NP-1012611.  
 XX (SOLV ) SOLVAY PHARM BV.  
 PA Deleersnijder W, Nys G, Zhang F;  
 PI WPI; 2001-182942/19.  
 DR N-PSDB; AAF56818.

XX Novel human G-protein coupled receptor family polypeptide, IGSL, useful  
 PT for treating psychiatric and central nervous system disorders such as  
 PT tics, tremor, Tourette's syndrome and Parkinson's disease -  
 XX Claim 15; Page 7; 65pp; English.

CC This represents a G-protein coupled receptor family polypeptide, IGSL.  
 CC The IGSL protein can be expressed by standard recombinant methodology.  
 CC IGSL is useful for inducing immunological response in a mammal, as  
 CC vaccine. IGSL polynucleotides and polypeptides and its modulators are  
 CC useful for treating psychiatric and central nervous system disorders  
 CC especially for movement disorders, such as tics, tremor, Tourette's syndrome,  
 CC Parkinson's disease, Huntington's disease, dyskinesias, dystonia and  
 CC spasms.

XX Sequence 508 AA;  
 SQ

Query Match 99.7%; Score 2637; DB 22; Length 508;  
 Best Local Similarity 99.8%; Pred. No. 1.5e-233;  
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60  
 DB 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60  
 QY 61 QLLQVTRNFIFNLVLTDLQISLVAAPVAVTSVPLFPLNSHFTALVSLTHLFAFASVN 120  
 DB 61 QLLQVTRNFIFNLVLTDLQISLVAAPVAVTSVPLFPLNSHFTALVSLTHLFAFASVN 120  
 QY 121 TIVLVSDRYLSTIHPILSPYSKMTQRRGYLLTGWTVAIIQSTPPLXGMOAFAFDRNA 180  
 DB 121 TIVLVSDRYLSTIHPILSPYSKMTQRRGYLLTGWTVAIIQSTPPLXGMOAFAFDRNA 180  
 QY 181 LCSMIMGASPSYTLISVSVFIVPLIYMIACYSVFCARROHALLVNRKHSLEVRKD 240  
 DB 181 LCSMIMGASPSYTLISVSVFIVPLIYMIACYSVFCARROHALLVNRKHSLEVRKD 240  
 QY 241 CVENEDDEGAKEKEEFODESEFRQHGHEVYKAKGRMEAKDGLAKEGSTGTSSEVYA 300  
 DB 241 CVENEDDEGAKEKEEFODESEFRQHGHEVYKAKGRMEAKDGLAKEGSTGTSSEVYA 300  
 QY 301 RGSEEVRESSSTVASDGSMEGKEGSTKYEENSMKADKGRTEVNOCSIDLGEDDMFEGDDI 360  
 DB 301 RGSEEVRESSSTVASDGSMEGKEGSTKYEENSMKADKGRTEVNOCSIDLGEDDMFEGDDI 360  
 QY 361 NFSEDDEAVANIPESLPPSRNSNSNPPLRCYCCKAKAVIFIIIFSVYLSLGPYCFLAY 420  
 DB 361 NFSEDDEAVANIPESLPPSRNSNSNPPLRCYCCKAKAVIFIIIFSVYLSLGPYCFLAY 420  
 QY 421 LAAWVDEVETQVQWVITIIILFLLQCCIHPIYVGYMHTIKKEIDMLKKFCKEKP 480  
 DB 421 LAAWVDEVETQVQWVITIIILFLLQCCIHPIYVGYMHTIKKEIDMLKKFCKEKP 480  
 QY 481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508  
 DB 481 EDSHPDLPGTEGGTEGKIVPSYDSATFP 508

RESULT 7  
 AAU04384  
 ID AAU04384 standard; protein: 508 AA.  
 AC AAU04384;  
 XX 23-OCT-2001 (first entry)  
 DE Human G-protein coupled receptor, hRUP15, mutant A398K.  
 KW Human; G-protein coupled receptor; GPCR; hRUP15; agonist;  
 inverse agonist; lung cancer; A398K; mutant; mutuin.  
 OS Homo sapiens.

```

XX  WO200136471-A2.
PN
XX
XX  25-MAY-2001.
PD
XX
XX  16-NOV-2000; 2000MO-USJ1509.
PF
XX
XX  17-NOV-1999; 99US-0166088.
PR
XX  17-NOV-1999; 99US-0166099.
PR
XX  17-NOV-1999; 99US-0166369.
PR
XX  23-DEC-1999; 99US-0171900.
PR
XX  23-DEC-1999; 99US-0171901.
PR
XX  23-DEC-1999; 99US-0171902.
PR
XX  11-FEB-2000; 2000US-0181749.
PR
XX  14-MAR-2000; 2000US-0189258.
PR
XX  14-MAR-2000; 2000US-0189259.
PR
XX  10-APR-2000; 2000US-0195898.
PR
XX  10-APR-2000; 2000US-0195899.
PR
XX  10-APR-2000; 2000US-0196078.
PR
XX  28-APR-2000; 2000US-0200419.
PR
XX  12-MAY-2000; 2000US-0203630.
PR
XX  12-JUN-2000; 2000US-0210741.
PR
XX  12-JUN-2000; 2000US-0210982.
PR
XX  21-AUG-2000; 2000US-0226760.
PR
XX  26-SEP-2000; 2000US-0235418.
PR
XX  26-SEP-2000; 2000US-0235779.
PR
XX  20-OCT-2000; 2000US-0242332.
PR
XX  20-OCT-2000; 2000US-0242343.
XX
XX  (AREN-) ARENA PHARM INC.
XX
XX  Chen R, Dang HT, Lowitz KP:
XX
XX  WPI: 2001-355616/37.
XX
XX  N-PSDB; AAS08265.
XX
XX  Endogenous and non-endogenous versions of human G-protein coupled
XX  receptors for direct identification of candidate compounds as agonists,
XX  inverse agonists or partial agonists for use as therapeutic agents -
XX
XX  Claim 30; Page 141; 160pp; English.
XX
XX  The sequence is a human G-protein coupled receptor (GPCR), hRUP15, mutant
XX  A398K. The endogenous and non-endogenous, constitutively activated
XX  versions of human G-protein coupled receptors (GPCR), are useful for
XX  direct identification of candidate compounds as receptor agonists.
XX  Inverse agonists or partial agonists having applicability as therapeutic
XX  agents for treating diseases related to GPCR, e.g. lung cancer.
XX  Non-endogenous version of human GPCRs are also utilized in research
XX  settings and in vitro and in vivo system, incorporating GPCRs can be
XX  utilized to elucidate and understand the roles these receptors
XX  play in the human condition, both normal and diseased.
XX
XX  Sequence 508 AA:
SQ
XX
XX  Query Match 99.7%; Score 2636; DB 22; Length 508;
XX  Best Local Similarity 99.6%; Pred. No. 1,9e-233;
XX  Matches 506; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX  1 MTSTCTSTRESSNSHTCMPLSKMPISLALGITSVLYFLAASVGNVYALVLRKP 60
XX  1 MTSTCTSTRESSNSHTCMPLSKMPISLALGITSVLYFLAASVGNVYALVLRKP 60
XX
XX  61 QLLQVTRRFNLLVPLDLSICVAPVNVATSVPLFWPLNSHCTALVSLTHFAFASVN 120
XX  61 QLLQVTRRFNLLVPLDLSICVAPVNVATSVPLFWPLNSHCTALVSLTHFAFASVN 120
XX
XX  121 TIVLVSVDRYLSITHTPLSYSPKMTORRGYLLTGTVIAVILQSTPPYLGMOAFAFDERNA 180
XX  121 TIVLVSVDRYLSITHTPLSYSPKMTORRGYLLTGTVIAVILQSTPPYLGMOAFAFDERNA 180
XX
XX  181 LCSMIMGASPSYTLISVVSFIVIPLIYMIACYSVVFCAARRQHALLVNKRHSLEVRKD 240
XX  181 LCSMIMGASPSYTLISVVSFIVIPLIYMIACYSVVFCAARRQHALLVNKRHSLEVRKD 240
XX

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Db  181 LCSMIMGASPSYTLISVVSFIVIPLIYMIACYSVVFCAARRQHALLVNKRHSLEVRKD 240
Oy  241 CVENEDEGAKEKKEFODESEFFRQHEGEYAKGEMAKDGSLSKAKEGSGTSESSVEA 300
Db  241 CVENEDEGAKEKKEFODESEFFRQHEGEYAKGEMAKDGSLSKAKEGSGTSESSVEA 300
Oy  301 RGSEVERESSVASDGSMEKGEKSTKVEENSMKADKRGTEVNOCSIDLGEDDMFEGDDI 360
Db  301 RGSEVERESSVASDGSMEKGEKSTKVEENSMKADKRGTEVNOCSIDLGEDDMFEGDDI 360
Oy  361 NFESEDDVEAVNIPESLPPSRNSNSNPPLPRCYCCAKAKVFIIFISYVLSLGPYCLAV 420
Db  361 NFESEDDVEAVNIPESLPPSRNSNSNPPLPRCYCCAKAKVFIIFISYVLSLGPYCLAV 420
Oy  421 LAVWVDVETQVPOKVTITITLFFLOCCIPHYVYGVMHTKKEIDOMLKKFCKEKP 480
Db  421 LAVWVDVETQVPOKVTITITLFFLOCCIPHYVYGVMHTKKEIDOMLKKFCKEKP 480
Oy  481 EDSHPDLPGTEGTEGKIVPSYDSATPP 508
Db  481 EDSHPDLPGTEGTEGKIVPSYDSATPP 508
XX
XX  RESULT 8
XX  AAU25561 standard; Protein: 204 AA.
XX
XX  AAU25561;
XX
XX  18-DEC-2001 (first entry)
XX
XX  Human G Protein-Coupled Receptor (GPCR) polypeptide #8.
XX
XX  Human: G-protein coupled receptor; GPCR: mental disorder; schizophrenia;
XX  attention deficit disorder; anxiety; depression; bipolar disorder;
XX  neurological disorder; Huntington's disease; dementia; obesity; anorexia;
XX  metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
XX  type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
XX  cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
XX  viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;
XX  antidepressant; anorectic; gene therapy.
XX
XX  Homo sapiens.
XX
XX  WO200162797-A2.
XX
XX  30-AUG-2001.
XX
XX  23-FEB-2001; 2001MO-US05676.
XX
XX  23-FEB-2000; 2000US-0184247.
XX  23-FEB-2000; 2000US-0184303.
XX  23-FEB-2000; 2000US-0184304.
XX  23-FEB-2000; 2000US-0184305.
XX  23-FEB-2000; 2000US-0184397.
XX  02-MAR-2000; 2000US-0186457.
XX  03-MAR-2000; 2000US-0186810.
XX  09-MAR-2000; 2000US-0188064.
XX  13-MAR-2000; 2000US-0188880.
XX  03-APR-2000; 2000US-0194344.
XX  23-JUN-2000; 2000US-0213861.
XX  11-JUL-2000; 2000US-0217369.
XX  11-JUL-2000; 2000US-0217370.
XX  14-JUL-2000; 2000US-0218337.
XX  20-JUL-2000; 2000US-0218492.
XX
XX  (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX  Vogeli G, Wood LS, Parodi LA, Land P;
XX
XX  WPI: 2001-570628/64.
XX
XX  N-PSDB; AAS42813.
XX

```



PT New isolated nucleic acid encoding a new G-protein coupled receptor  
PT polypeptide for detecting receptor modulators that can treat mental  
PT disorders, such as schizophrenia, anxiety, depression, or obesity -  
XX  
PS Claim 35; Page 73; 279pp; English.  
XX  
CC Sequences AAU2554-AAU25616 represent human G-protein coupled receptor  
CC (GPCR) polypeptides of the invention. The proteins and their associated  
CC DNA sequences can be used to identify compounds which bind to GPCR  
CC polypeptides and in screening for compounds that modulate GPCR activity.  
CC By screening a human subject for the presence of mutations in GPCR DNA, a  
CC GPCR-related disorder or a genetic predisposition can be diagnosed. The  
CC sequences can also be used for treatment and prevention of mental  
CC disorders such as schizophrenia, attention deficit disorder, anxiety,  
CC depression, dementia and bipolar disorder, neurological disorders such as  
CC Huntington's disease, Parkinson's disease and Tourette's syndrome,  
CC metabolic disorders such as obesity, anorexia and type 2 diabetes,  
CC cardiovascular disorders such as thrombosis, myocardial infarction,  
CC cardiomyopathy and atherosclerosis, viral infections caused by HIV and  
CC cancers.  
CC  
SQ Sequence 204 AA:  
XX  
Query Match 29.9%; Score 791; DB 22; Length 204;  
Best Local Similarity 98.7%; Pred. No. 1.6e-64;  
Matches 156; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MTSTCNSTRESNSHTCMPLSKMPISLANGITRSTVLTFLAASFGNVLALVLRKP 60  
DB 47 MTSTCNSTRESNSHTCMPLSKMPISLANGITRSTVLTFLAASFGNVLALVLRKP 106  
QY 61 QLLQVTRFNFNLVTDLQISLVAPVWVATSVLPFWLNSHCTALVSLTHLFAFASV 120  
DB 107 QLLQVTRFNFNLVTDLQISLVAPVWVATSVLPFWLNSHCTALVSLTHLFAFASV 166  
QY 121 TIVLVSVDRYLSIHLPSYPSKMTORRGYLLVGTWIV 158  
DB 167 TIVLVSVDRYLSIHLPSYPSKMTORRGYLLVGTWIV 204  
XX  
RESULT 9  
AA70343  
ID AA70343 standard; Protein; 407 AA.  
XX  
AC AA70343;  
XX  
DT 20-JUN-2000 (first entry)  
XX  
DE Human G protein-coupled orphan receptor, RE2.  
XX  
KM G protein-coupled orphan receptor; GPCR; agonist; G protein; treatment;  
XX GPCR fusion protein; Inverse agonist; drug; RE2; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200006597-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 30-JUL-1999; 99WO-US17425.  
XX  
PR 31-JUL-1998; 98US-0094879.  
PR 30-OCT-1998; 98US-0106300.  
PR 04-DEC-1998; 98US-0110906.  
PR 26-FEB-1999; 99US-0121851.  
XX  
PA (AREN-) ARENA PHARM INC.  
XX  
PI Behan DP, Chalmers DT, Liaw C, Lin I, Lowitz K, Chen R;  
XX WPI; 2000-195260/17.  
XX DR N-PSDB; AA51461.  
XX

PT Identification of a compound useful as a therapeutic agent, comprises  
PT identifying a compound against constitutively activated G  
PT protein-coupled orphan receptors -  
XX  
PS Example 2; Page 111; 123pp; English.  
XX  
CC The patent discloses a method of identifying agonists and inverse or  
CC partial agonists to the endogenous, constitutively activated  
CC G protein-coupled orphan receptors (GPCRs), by contacting them with a  
CC GPCR fusion protein comprising a GPCR and a G protein. Determining  
CC expression of GPCRs in tissue samples can be used to identify related  
CC diseases. Inverse agonists to these receptors can be used as drugs for  
CC treating GPCR-related diseases. The present protein sequence is that of  
CC human G protein-coupled orphan receptor, RE2.  
XX  
SQ Sequence 407 AA:  
XX  
Query Match 14.8%; Score 391; DB 21; Length 407;  
Best Local Similarity 23.6%; Pred. No. 2.3e-27;  
Matches 106; Conservative 67; Mismatches 130; Indels 146; Gaps 11;  
QY 31 GIIRSTVLTFLAASV--GNIVLALVLRKPQLQVTRFNFNLVTDLQISLVAPW 88  
DB 25 GVITTFIATIVITIFVCLGNLVITVLYKRSYLLTSLNKFVSLTNFLSVLPFV 84  
QY 89 VNTSVLPFWLNSHCTALVSLTHLFAFASVNTIVLVSVDRYLSIHLPSYPSKMTORRG 148  
DB 85 VTSSIRREWFNGVWCFNSALLYLTLISSASMTLGVIAIDRYAVLVPMVPMKITGNRA 144  
QY 149 YLLVYGTWIVAILOSTPPLGLWGQAFDERNALCSMTWASPSYTLISVSVFIYPLIM 208  
DB 145 VMLVYITWMLSHLQCLPPLGLWGSVEFERKMCVAMHREPGTAWQIMCALFFPLV 204  
QY 209 IACYSVFCAARHALLVYKRSLEVRVYKDCVENEDEGAEEKKEEFQDESEFRROHEG 268  
DB 205 LVYCGEYFVRAR-----VKARKVHCGTVIYE-BDAO----- 235  
QY 269 EVKAKKEGRMEKKSOLKAKGSGTSGTSSEVBARSESEVRRESSYVASGSMCKGKSTKYE 328  
DB 236 ---RTGR-----KNSSTSTSSG----- 250  
QY 329 ENSMKADKGRTEVNOCSIDGEDDMERGEDDINESEDDVAVNIPESLPSRRNS----- 383  
DB 251 -----SRRNAPGVV 260  
QY 384 -NSNPPLRCYQCKAAVFIILIFSIVLSLGPY-CFLAVLAW--VDVETQVPMQVITTI 439  
DB 261 YSAN-----QCKALITILVLGAFVWTGMPYVWVIASEALMCKSSVSPSLFTWA----- 309  
QY 440 IWLFFLOCCIHPRVYGYGMHKTIRKEIOM 468  
DB 310 TWLSFASAVCHPLIYGLMNTVRKELLGM 338  
XX  
RESULT 10  
AAW58586  
ID AAW58586 standard; Protein; 454 AA.  
XX  
AC AAW58586;  
XX  
DT 07-SEP-1998 (first entry)  
XX  
DE Human histamine H2 receptor.  
XX  
KM Human; histamine H2 receptor; H2RH; inflammatory disease; gastric;  
XX nervous condition.  
XX  
OS Homo sapiens.  
XX  
PN WO9820040-A1.  
XX WPI; 14-MAY-1998.  
XX



```

Db 274 ----- 273
Oy 364 EDDVEAVNIPESLPSPRRNS-----NSNPPLPRCYQCKAAKAVFIITIFSYLSIGPY-C 416
Db 274 -----SRRNAFGGVVYSAN-----QCKALITLIVLGAFWVTGWPYMW 311
Oy 417 FLAVLAW--VDVETQVPQWVITIIIMLFLLQCCIHPPYVGYMHTIKKEIQDM 468
Db 312 VIASEALMGKSSVSPSLETMA---TWLSFASAVCHSLIYGLMNTVKRELLGM 361

RESULT 12
AAR90989
ID AAR90989 standard; Protein: 529 AA.
AC AAR90989;
XX 27-MAY-1996 (first entry)
DT
XX
DE Human adrenergic G-protein coupled receptor.
XX
XX G-protein coupled receptor polypeptide; GCRP; adrenergic receptor;
XX agonist; antagonist; therapy; hypertension; respiratory disease.
XX
XX Homo sapiens.
XX
XX MO9605225-A1.
XX
XX 22-FEB-1996.
XX
XX 10-AUG-1994; 94WO-US09051.
XX
XX 10-AUG-1994; 94WO-US09051.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PA
XX PI Adams MD, LI Y, Soppet DR;
XX
XX WPI; 1996-139642/14.
XX
XX N-PSDB; AAT13002.
XX
XX
XX New isolated G-protein coupled receptor polypeptide - used to
XX develop prods. to inhibit or stimulate adrenergic receptors for
XX treating e.g. hypertension or respiratory disorders
XX
XX Claim 4; Fig 1; 60pp; English.
XX
XX Human G-protein coupled receptor polypeptide (GCRP) (AAR90989)
XX is a protein structurally related to the alpha-1 adrenergic
XX receptor family. It can be produced by expression of a cDNA clone
XX (AAT13002) isolated from a human infant brain cDNA library.
XX Recombinant GCRP is used to screen for agonist and antagonist
XX cpts. useful e.g. in the treatment of hypertension and respiratory
XX disorders, and to raise anti-GCRP antibodies.
XX
XX
XX Sequence 529 AA;

Query Match 14.0%; Score 371; DB 17; Length 529;
Best Local Similarity 23.1%; Pred. No. 2,2e-25;
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;

```

```

Oy 181 LCSMTMGASPSYTIILSVSFIVIPLIIMACYSVYECARBOHALLYNKRHSLEVRKD 240
Db 177 MCVAAAMHREPGYTAAWQIMCAIFPPLVIMVCGIFRVAR-----VKARKHCGTIV 228
Oy 241 CVENDEDEGAKEKEEFODESEFRROHEGEVAKESGRMEAKDGLKAKEGSTGTSSESYEA 300
Db 229 IVE-EDAQ-----RIGR-----KNSSTSTSS----- 249
Oy 301 RGESEVRRESSIVASDGMEGKEGSTEVENSKADKRTENVQCSIDLGEDDMFEGDDI 360
Db 250 -----GR----- 251
Oy 361 NFSEDDVEAVNIPESLPSPRRNS-----NSNPPLPRCYQCKAAKAVFIITIFSYLSIGP 414
Db 252 -----SRRNAFGGVVYSAN-----QCKALITLIVLGAFWVTGWP 285
Oy 415 Y-CFLAVLAW--VDVETQVPQWVITIIIMLFLLQCCIHPPYVGYMHTIKKEIQDM 468
Db 286 YMWVVIASEALMGKSSVSPSLETMA---TWLSFASAVCHSLIYGLMNTVKRELLGM 338

RESULT 13
AAM70501
ID AAM70501 standard; Protein: 529 AA.
AC AAM70501;
XX 29-DEC-1998 (first entry)
DT
XX
DE Human G-protein adrenergic receptor protein sequence.
XX
XX Human G-protein adrenergic receptor; baculovirus expression system;
XX COS cell; upper respiratory condition; hypertension.
XX
XX Homo sapiens.
XX
XX US5817477-A.
XX
XX 06-OCT-1998.
XX
XX 06-JUN-1995; 95US-0467568.
XX
XX 06-JUN-1995; 95US-0467568.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PA
XX PI Adams MD, LI Y, Soppet DR;
XX
XX WPI; 1998-556386/47.
XX
XX N-PSDB; AAV33510.
XX
XX
XX DNA encoding adrenergic receptor polypeptide - useful for producing
XX recombinant polypeptide and identifying antagonists and agonists of
XX the receptor
XX
XX Claim 1; Fig 1A-1E; 38pp; English.
XX
XX The present DNA sequence represents a human G-protein adrenergic receptor
XX protein sequence. The receptor is encoded by DNA isolated from a human
XX infant cDNA library. Vectors and host cells (e.g. Baculovirus expression
XX system, COS cells, etc.) can be used for recombinant production of the
XX receptor. The recombinant receptor is claimed to be useful for
XX identifying antagonists and agonists of the receptor, and for raising
XX antibodies against it. The agonists are claimed useful for treating
XX disease conditions associated with the receptor activity, e.g upper
XX respiratory conditions and hypertension.
XX
XX
XX Sequence 529 AA;

Query Match 14.0%; Score 371; DB 19; Length 529;
Best Local Similarity 23.1%; Pred. No. 2,2e-25;
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:45:08 ; Search time 16 Seconds  
(without alignments)  
775.513 Million cell updates/sec

Title: US-09-992-238-2

Perfect score: 2644  
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Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/PCtUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	388.5	14.7	454	2	US-08-748-485-1 Sequence 1, Appl
2	371	14.0	529	2	US-08-467-568-2 Sequence 2, Appl
3	371	14.0	529	5	PCT-US94-09051-2 Sequence 2, Appl
4	371	14.0	529	5	PCT-US94-09051-2 Sequence 2, Appl
5	343.5	13.0	422	1	US-07-817-920-3 Sequence 3, Appl
6	343.5	13.0	422	1	US-08-370-542-3 Sequence 3, Appl
7	343.5	13.0	422	1	US-08-117-006-3 Sequence 3, Appl
8	343.5	13.0	422	1	US-08-216-594-3 Sequence 3, Appl
9	343.5	13.0	422	1	US-08-542-358-3 Sequence 3, Appl
10	343.5	13.0	422	2	US-08-157-185-13 Sequence 13, Appl
11	343.5	13.0	422	3	US-08-281-5268-13 Sequence 13, Appl
12	343.5	13.0	422	3	US-09-018-351-3 Sequence 3, Appl
13	343.5	13.0	422	5	PCT-US93-00149-3 Sequence 3, Appl
14	338.5	12.8	466	1	US-08-334-698-6 Sequence 6, Appl
15	338.5	12.8	466	1	US-08-228-932-6 Sequence 6, Appl
16	338.5	12.8	466	1	US-08-468-939-6 Sequence 6, Appl
17	338.5	12.8	466	1	US-08-722-001-28 Sequence 28, Appl
18	338.5	12.8	466	2	US-08-406-855A-6 Sequence 6, Appl
19	338.5	12.8	466	2	US-08-722-190-6 Sequence 6, Appl
20	338.5	12.8	466	3	US-08-244-354-6 Sequence 6, Appl
21	338.5	12.8	466	5	PCT-US95-04203-6 Sequence 6, Appl
22	338.5	12.8	466	5	PCT-US95-04203-6 Sequence 6, Appl
23	333.5	12.6	429	2	US-08-748-485-7 Sequence 7, Appl
24	333.5	12.6	466	1	US-08-722-001-12 Sequence 12, Appl
25	333.5	12.6	466	2	US-08-467-568-11 Sequence 11, Appl
26	333.5	12.6	466	2	US-09-030-582-11 Sequence 11, Appl
27	324.5	12.3	466	2	US-08-406-855A-23 Sequence 23, Appl

28	324.5	12.3	466	3	US-09-206-899-23 Sequence 23, Appl
29	314.5	11.9	501	1	US-08-722-001-14 Sequence 14, Appl
30	314.5	11.9	501	2	US-08-467-568-9 Sequence 9, Appl
31	314.5	11.9	501	2	US-09-030-582-9 Sequence 9, Appl
32	314.5	11.9	572	1	US-08-334-698-2 Sequence 2, Appl
33	314.5	11.9	572	1	US-08-228-932-2 Sequence 2, Appl
34	314.5	11.9	572	1	US-08-468-939-2 Sequence 2, Appl
35	314.5	11.9	572	1	US-08-722-001-30 Sequence 30, Appl
36	314.5	11.9	572	2	US-08-406-855A-2 Sequence 2, Appl
37	314.5	11.9	572	2	US-08-722-190-2 Sequence 2, Appl
38	314.5	11.9	572	3	US-08-244-354-2 Sequence 2, Appl
39	314.5	11.9	572	3	US-09-206-899-2 Sequence 2, Appl
40	314.5	11.9	572	5	PCT-US95-04203-2 Sequence 2, Appl
41	309.5	11.7	521	2	US-08-406-855A-19 Sequence 19, Appl
42	309.5	11.7	521	3	US-09-206-899-19 Sequence 19, Appl
43	304.5	11.5	601	1	US-07-676-174A-2 Sequence 2, Appl
44	302.5	11.4	375	1	US-08-118-270-17 Sequence 17, Appl
45	302.5	11.4	375	5	PCT-US93-08528-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-08-748-485-1  
Sequence 1, Application US/08748485  
Patent No. 5817480  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Goli, Surya K.  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,485  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0159 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 454 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Consensus  
CLONE: 1722180  
US-08-748-485-1  
Query Match 14.7%, Score 388.5, DB 2, Length 454;





TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 529 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-030-582-2

Query Match 14.0%; Score 371; DB 2; Length 529;  
Best Local Similarity 23.1%; Pred. No. 3.3e-22;  
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;

QY 6 TNSTRE-----SNSHTCMPLSKMPISLHGIIRSTVLVIFLASFGVGNVLAIVLQRP 60  
DB 14 SNTLEEGGCGASSPSSPSSLSPP-----FLSA--WGNLVIVVTLTKKS 56  
QY 61 QLLQVTRFTFNLVTDLLQISLAPVAVATSVPLFWPLNSHCTALVSLTHLFAFASVN 120  
DB 57 YLLTSLKKEFVSLTSLNPLSVLPLPVVTSIRREMIPEGVWCMNFSAIYLLTSSASML 116  
QY 121 TIVLVSVDRSLTIHPILSYSKMTORRGYLLTGTVIAIIGSTPPLYGNGQAADERNA 180  
DB 117 TLGVIAIDRYAVLYPWPYPMKITGNRAVALYIMLSLIGCLPLFGSSVEYGENKW 176  
QY 181 LGSIMWASPSYTLISVSVFTIPLIYMIACYSVFCARQHALLYNKRHSLEVRKD 240  
DB 177 MCVAAWHREGYTAFWQIMCALPEFLVLCYGFIFRVAR-----VARKVHCCTVV 228  
QY 241 CVENEDEGAKEKKEFODESEFRQHEGEVAKAGRMKADGSLAKEGSTGTSSEVEA 300  
DB 229 IVE-EDAQ-----RTGR-----KNSSTSTSSS-----249  
QY 301 RGSEEVRESSTVASDGSMEGKSTKVEENSMKADGRTEVNCISIDLGEDDMFEGDDI 360  
DB 250 -----GR-----251  
QY 361 NFSEDDVEAVNIPESLPSPRRNS-----NSNPPLPRCYOCKAKAVIFIIIFSVLSLP 414  
DB 252 -----RRNAFQGVVYSAN-----OCKALITLIVLGAFAWVTWGP 285  
QY 415 Y-CFLAVLAWV--VDVETQVPQWVITIIIMLFLOCCIHPPVYGYMKHTIKKEIQDM 468  
DB 286 YMVVIASEALMGKSSVPSLETWA---TWLSFASAVCHPLITGLMKNKTVRKELLGM 338

RESULT 4  
PCT-US94-09051-2  
Sequence 2, Application PC/TUS9409051  
GENERAL INFORMATION:  
APPLICANT: LI, ET AL.  
TITLE OF INVENTION: Adrenergic Receptor  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09051  
FILING DATE: Submitted herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-194  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 529 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
PCT-US94-09051-2

Query Match 14.0%; Score 371; DB 5; Length 529;  
Best Local Similarity 23.1%; Pred. No. 3.3e-22;  
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;

QY 6 TNSTRE-----SNSHTCMPLSKMPISLHGIIRSTVLVIFLASFGVGNVLAIVLQRP 60  
DB 14 SNTLEEGGCGASSPSSPSSLSPP-----FLSA--WGNLVIVVTLTKKS 56  
QY 61 QLLQVTRFTFNLVTDLLQISLAPVAVATSVPLFWPLNSHCTALVSLTHLFAFASVN 120  
DB 57 YLLTSLKKEFVSLTSLNPLSVLPLPVVTSIRREMIPEGVWCMNFSAIYLLTSSASML 116  
QY 121 TIVLVSVDRSLTIHPILSYSKMTORRGYLLTGTVIAIIGSTPPLYGNGQAADERNA 180  
DB 117 TLGVIAIDRYAVLYPWPYPMKITGNRAVALYIMLSLIGCLPLFGSSVEYGENKW 176  
QY 181 LGSIMWASPSYTLISVSVFTIPLIYMIACYSVFCARQHALLYNKRHSLEVRKD 240  
DB 177 MCVAAWHREGYTAFWQIMCALPEFLVLCYGFIFRVAR-----VARKVHCCTVV 228  
QY 241 CVENEDEGAKEKKEFODESEFRQHEGEVAKAGRMKADGSLAKEGSTGTSSEVEA 300  
DB 229 IVE-EDAQ-----RTGR-----KNSSTSTSSS-----249  
QY 301 RGSEEVRESSTVASDGSMEGKSTKVEENSMKADGRTEVNCISIDLGEDDMFEGDDI 360  
DB 250 -----GR-----251  
QY 361 NFSEDDVEAVNIPESLPSPRRNS-----NSNPPLPRCYOCKAKAVIFIIIFSVLSLP 414  
DB 252 -----RRNAFQGVVYSAN-----OCKALITLIVLGAFAWVTWGP 285  
QY 415 Y-CFLAVLAWV--VDVETQVPQWVITIIIMLFLOCCIHPPVYGYMKHTIKKEIQDM 468  
DB 286 YMVVIASEALMGKSSVPSLETWA---TWLSFASAVCHPLITGLMKNKTVRKELLGM 338

RESULT 5  
US-07-817-920-3  
Sequence 3, Application US/07817920  
Patent No. 5360735  
GENERAL INFORMATION:  
APPLICANT: Weinsbank, Richard L  
APPLICANT: Branchek, Theresa  
APPLICANT: Hartig, Paul R  
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:



QY 377 PPSRRNSNPLPRCYOAKAVYFIIFSVLSGPGFLAVLAVVDETQVPOWVI 436  
 Db 323 RKNERNNAEAKRMALAREKTYKTLIGITMGTFILCMLPEFFVALVLPCESSCHMPTLLG 382  
 QY 437 TTIWLFLOCCIHPIYGYVMHKTIKKEIODMLKKFPCKE 476  
 Db 383 AIIWMLGYSNLSLNPVITAYFNKDFQNAFKKIICLPCFRQ 422

## RESULT 7

US-08-117-006-3  
 ; Sequence 3, Application US/08117006  
 ; Patent No. 5639652  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weinshank, Richard L.  
 ; APPLICANT: Branchek, Theresa  
 ; APPLICANT: Hartig, Paul R.  
 ; TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND  
 ; TITLE OF INVENTION: USES THEREOF  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10112  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Wordperfect, Version 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/117, 006  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 1795/39318  
 ; TELEPHONE: 212-977-9550  
 ; TELEFAX: 212-664-0525  
 ; TELEX: 422523 COOP UI  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 422 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 ; IMMEDIATE SOURCE:  
 ; CLONE: 5-HT1A  
 ; US-08-117-006-3

Query Match 13.0%; Score 343.5; DB 1; Length 422;  
 Best Local Similarity 22.0%; Pred. No. 4,1e-20;  
 Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLAHGIRSTVIVLFLAASVGN-IVLALVLORRQPOLLOVTRNFIENLVLVTLQISL 83  
 Db 31 VTASYQVITSLTLGLFCALVGNACVAAIALER--SLQWVANVLLIGSLAVTDLMASVL 88  
 QY 84 VAPWVAATSVPLFPINSHFCTALVSLHLFAFASVNTIVLVSQRYLSIIHPLSPSKM 143  
 Db 89 VLPMAALYQVINKKTLGQVTDLPALDVLCTSSILHLCAIADRWYAITDPIDYVNR 148  
 QY 144 TORRGYLLYGTWIVAIQISTPPPLYGMOQAADFERNALCSMIWASPSYTIISVVSFVI 203

Db 149 TPRAAALISLTLGLFLISIPMLGMWRT--EDRSDPDACIISKDHGYTIYTFGAFYI 206  
 QY 204 PLIVNIACYSVFECARQHALIVVKKRHSLEVRKDCVENDEGAKKEPFQDESEFR 263  
 Db 207 PLLMLVLYGRIFRAAR-----FRIRKTVKKVEKYGADTRHGSAPAPPK 251  
 QY 264 ROHEGEVAKREGM--EAKDGL-----KAKEGSTGSESSVEARGSEVRSSVVASDG 316  
 Db 252 KSVNGESGSRNKRGLVESKAGALCANAVROGDGALLEVIVH----- 296  
 QY 317 SMEKREGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEDDINFSDVEAVNIPESL 376  
 Db 297 ---RVGNSK-EHLPLPSEAGPTPCAPASFE----- 322  
 QY 377 PPSRRNSNPLPRCYOAKAVYFIIFSVLSGPGFLAVLAVVDETQVPOWVI 436  
 Db 323 RKNERNNAEAKRMALAREKTYKTLIGITMGTFILCMLPEFFVALVLPCESSCHMPTLLG 382  
 QY 437 TTIWLFLOCCIHPIYGYVMHKTIKKEIODMLKKFPCKE 476  
 Db 383 AIIWMLGYSNLSLNPVITAYFNKDFQNAFKKIICLPCFRQ 422

## RESULT 8

US-08-216-594-3  
 ; Sequence 3, Application US/08216594  
 ; Patent No. 5652113  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weinshank, Richard L.  
 ; APPLICANT: Branchek, Theresa  
 ; APPLICANT: Hartig, Paul R.  
 ; TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10112  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/216, 594  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 1795/39318  
 ; TELEPHONE: 212-977-9550  
 ; TELEFAX: 212-664-0525  
 ; TELEX: 422523 COOP UI  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 422 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 ; IMMEDIATE SOURCE:  
 ; CLONE: 5-HT1A  
 ; US-08-216-594-3

Query Match 13.0%; Score 343.5; DB 1; Length 422;  
 US-08-216-594-3



NAME: White P., John  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 41908-A-PCT-US/JPW/MAT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 422 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-157-185-13

Query Match 13.0%; Score 343.5; DB 2; Length 422;  
 Best Local Similarity 22.0%; Pred. No. 4.1e-20;  
 Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLAHGIRSVLYIFLAASFGN--IYLAIVLQRPOLLQVTRFENLVTDLQISL 83  
 Db 31 VTSYQVITSLILGLTIFCAVGNACVAAIALER--SLQVANYLIGSLAVTDLMVSVL 88  
 QY 84 VAPWVATSVPLFMPNLSHFTALVSLHLFAPASVNTIVLSVDRYLSIHLPSYSKM 143  
 Db 89 VLPMAALYQVNLKWTGLQVTCDFIALDVLCTSSILHLCAIALDRYWAITDPIDYVKR 148  
 QY 144 TORRGYLLVGTWIVALLQSTPRPLXGWOAAFDERNALCSMIGWASPTTLVSFVI 203  
 Db 149 TPRRAALISLTWILGLIFSLIPMLGWRT--EDRSDPDCTISKDHYTYSFGAFYI 206  
 QY 204 PLIYMIACYSVFCARQAHLLYNKRHSLEVRKDCVENEDEGAKKEEFODESEFR 263  
 Db 207 PLILMLVLYGRIFRAAR-----FRIRKTVKVEKTGADTRGASAPAPQK 251  
 QY 264 ROHEGEVAKEGRM--EAKDGL-----KAKGSGTGSSEVSEARGSEVESSVASDG 316  
 Db 252 KSVNGESGRMWRIGVESKAGALCANGAVRQGDGALEVIYEH----- 296  
 QY 317 SMEKEGSTVEENSMKADKRTVEYNOCSDILGEDMEFGEDINFSEDDVEAVNIPESL 376  
 Db 297 ---RVNSK--EHLPLPSEAGPTPCAPASFE----- 322  
 QY 377 PPSRRNSNPPLPRCYQCAKAVIFITISVYLSLGPYCLAVLAWVDVETQVPMVI 436  
 Db 323 RKNERNAEARKKMLAREKTVKTLGITMGTFILCMLPFYVALVLPCESSCHMPTLLG 382  
 QY 437 TITIMLFLOCCIHPIYVYGYMHTIKKEIDMLKKEFCKE 476  
 Db 383 AIIIMLGYSNLNPVIYAFNKFQNAFKIICLCFCRQ 422

RESULT 11  
 US-08-281-526B-13  
 Sequence 13, Application US/08281526B  
 Patent No. 6083749  
 GENERAL INFORMATION:  
 APPLICANT: Bard A. Jonathan  
 APPLICANT: Branchek A. Theresa  
 APPLICANT: Weinsbank L. Richard  
 TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.24  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/281,526B  
 FILING DATE: 27-JUL-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White P., John  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 41908-1/JPW  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 422 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-281-526B-13

Query Match 13.0%; Score 343.5; DB 3; Length 422;  
 Best Local Similarity 22.0%; Pred. No. 4.1e-20;  
 Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLAHGIRSVLYIFLAASFGN--IYLAIVLQRPOLLQVTRFENLVTDLQISL 83  
 Db 31 VTSYQVITSLILGLTIFCAVGNACVAAIALER--SLQVANYLIGSLAVTDLMVSVL 88  
 QY 84 VAPWVATSVPLFMPNLSHFTALVSLHLFAPASVNTIVLSVDRYLSIHLPSYSKM 143  
 Db 89 VLPMAALYQVNLKWTGLQVTCDFIALDVLCTSSILHLCAIALDRYWAITDPIDYVKR 148  
 QY 144 TORRGYLLVGTWIVALLQSTPRPLXGWOAAFDERNALCSMIGWASPTTLVSFVI 203  
 Db 149 TPRRAALISLTWILGLIFSLIPMLGWRT--EDRSDPDCTISKDHYTYSFGAFYI 206  
 QY 204 PLIYMIACYSVFCARQAHLLYNKRHSLEVRKDCVENEDEGAKKEEFODESEFR 263  
 Db 207 PLILMLVLYGRIFRAAR-----FRIRKTVKVEKTGADTRGASAPAPQK 251  
 QY 264 ROHEGEVAKEGRM--EAKDGL-----KAKGSGTGSSEVSEARGSEVESSVASDG 316  
 Db 252 KSVNGESGRMWRIGVESKAGALCANGAVRQGDGALEVIYEH----- 296  
 QY 317 SMEKEGSTVEENSMKADKRTVEYNOCSDILGEDMEFGEDINFSEDDVEAVNIPESL 376  
 Db 297 ---RVNSK--EHLPLPSEAGPTPCAPASFE----- 322  
 QY 377 PPSRRNSNPPLPRCYQCAKAVIFITISVYLSLGPYCLAVLAWVDVETQVPMVI 436  
 Db 323 RKNERNAEARKKMLAREKTVKTLGITMGTFILCMLPFYVALVLPCESSCHMPTLLG 382  
 QY 437 TITIMLFLOCCIHPIYVYGYMHTIKKEIDMLKKEFCKE 476  
 Db 383 AIIIMLGYSNLNPVIYAFNKFQNAFKIICLCFCRQ 422

RESULT 12  
 US-09-018-351-3  
 Sequence 3, Application US/09018351  
 Patent No. 6096507  
 GENERAL INFORMATION:  
 APPLICANT: Weinsbank, Richard L.  
 APPLICANT: Branchek, Theresa  
 APPLICANT: Hartig, Paul R.  
 TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1E RECEPTOR  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/018.351  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/542.358  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1795/39317-22/JPM/MAT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 422 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-09-018-351-3

Query Match 13.0%; Score 343.5; DB 3; Length 422;  
Best Local Similarity 22.0%; Pred. No. 4.1e-20;  
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

26 ISLAHGIIIRSVLYIFLASVGN--IVLALVLRKPOLLOVTRFENLVTDLQISL 83  
31 VTTSYQVITSLTGLTFCAVLGNACVAAIALER--SLQNVANVLLGSLAVTDLMSVL 88  
84 VAPWVATSVPLFPLNSHFCALVSLTHLFAFASVNTIVLSYDRYLSIHPLSYPSKM 143  
89 VLPRMALYQVINKMTLQVTCDFIALDVLCCTSSILHCAIALDRWAIIDPIDYVKR 148  
144 TORRGYLLTGWTVAILOSTPPPLYGWGQAADERNALCSMIWASPSYTLISVVSFTVI 203  
149 TPRRAAALISLTWLIGFLISIPMLGWTRP--EDRSPDCACTISKDHGYTTSFGAFYI 206  
204 PLIYMIACYSVFCARQNALLVNKRHSLEVAVKDCVENEDEGAKEKKEPFDESEFR 263  
207 PLLMLVLVYGRIFRAAR-----FRIKRTVKKVEKTGADTRHGASPAQPK 251  
264 ROHGEVYAKAGRM--EAKDGL-----KAKEGSTGTSSESVFARGSEVEESSTVASDG 316  
252 KSVNGEGSRMRRLGVESKAGALCANGAVRQGDGALEVEVH----- 296  
317 SMEKEGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEDDINFSEDDVEAVNIPESL 376  
297 ---RVGNSK-EHPLPSEAGPTPCAPASFE----- 322  
377 PPSRRNSNSNPRLRCYQCKAKAYIFIIISYVSLGPRYCLAVLAVWVDVETQVQWVI 436  
323 RKNERNEAARKRMALARRKRVKTLGILMGFLICWLPFFTLVALVLDPESSCHMPTLLG 382  
437 TIIMLFELQCCIPHYVGYMHTIKKEIODMLKKFPCKE 476  
383 AIIMKLGYSNLNLPVITAYATFNKDPQNAFKIICLCRCRQ 422

RESULT 13

PCT-US93-00149-3  
Sequence 3, Application PC/TUS9300149  
GENERAL INFORMATION:  
APPLICANT: Weinsbank, Richard L.  
APPLICANT: Brantley, Theresa  
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/00149  
FILING DATE: 19930108  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1795/39318  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 422 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
IMMEDIATE SOURCE:  
CLONE: 5-HT1A  
PCT-US93-00149-3

Query Match 13.0%; Score 343.5; DB 5; Length 422;  
Best Local Similarity 22.0%; Pred. No. 4.1e-20;  
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

26 ISLAHGIIIRSVLYIFLASVGN--IVLALVLRKPOLLOVTRFENLVTDLQISL 83  
31 VTTSYQVITSLTGLTFCAVLGNACVAAIALER--SLQNVANVLLGSLAVTDLMSVL 88  
84 VAPWVATSVPLFPLNSHFCALVSLTHLFAFASVNTIVLSYDRYLSIHPLSYPSKM 143  
89 VLPRMALYQVINKMTLQVTCDFIALDVLCCTSSILHCAIALDRWAIIDPIDYVKR 148  
144 TORRGYLLTGWTVAILOSTPPPLYGWGQAADERNALCSMIWASPSYTLISVVSFTVI 203  
149 TPRRAAALISLTWLIGFLISIPMLGWTRP--EDRSPDCACTISKDHGYTTSFGAFYI 206  
204 PLIYMIACYSVFCARQNALLVNKRHSLEVAVKDCVENEDEGAKEKKEPFDESEFR 263  
207 PLLMLVLVYGRIFRAAR-----FRIKRTVKKVEKTGADTRHGASPAQPK 251  
264 ROHGEVYAKAGRM--EAKDGL-----KAKEGSTGTSSESVFARGSEVEESSTVASDG 316  
252 KSVNGEGSRMRRLGVESKAGALCANGAVRQGDGALEVEVH----- 296  
317 SMEKEGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEDDINFSEDDVEAVNIPESL 376

Db 297 ----RVGNSK-EHLPSEAGPTPCADAPSE----- 322

Qy 377 PPSRNSNSNPPLPRCOCRAKAVIFIIIFSVLSLGPYCFGLAVLAWVDVETQYPMVI 436

Db 323 KKNERNNAKKKMLAKERKVKTLGIIMGTFLCWLPEFIVLAVLPCESSCHMPTLLG 382

Qy 437 TIIMLFLOCCIHPIYVGYGMHTIKKEIODMLKKEFCKE 476

Db 383 AIIMWLGNSLNPVIYAFNKDFQNAFKKIICLCFCRQ 422

RESULT 14

US-08-334-698-6

Sequence 6, Application US/08334698

Patent No. 5556753

GENERAL INFORMATION:

APPLICANT: Jonathan A. Bard et al.

TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic

TITLE OF INVENTION: Receptors and Uses Thereof

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/334,698

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/952,798

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 376901

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: (212) 422523 COOP UI

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 466 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-334-698-6

Query Match 12.8%; Score 338.5; DB 1; Length 466;

Best Local Similarity 21.3%; Pred. No. 1.2e-19;

Matches 108; Conservative 80; Mismatches 187; Indels 131; Gaps 11;

Qy 8 STRESNSHRCMPKSPKIPSLAHGIIRSTVIVIFLAASFGVNIYALVLOKRPOLQVYN 67

Db 5 SGNASDSSNCRP--PAVNISSKAILLGVILGILFVGLNIIYILSVACHRHLSVTH 62

Qy 68 RFIFNLVTFDILQISLVAAPVAVATVPLEWPLNSHCTALVSLTHLFAFASVNTIVLVS 127

Db 63 YYIYNLAVADLLITSTVLPFSAIFEVLGVMFAGVFCNIMAAVDVLCCTASIMGLCTISI 122

Qy 128 DRYLSIIHPLSPSKMQRRCGYLLLYGWYVAILLOSTPPIYGMQGAARDERNALCSMTWG 187

Db 123 DRYGVSPLEKPYPIYVQRGIMALLCWMALSLVISISGLPFGWRQPA--PEDETTICQI--N 179

Qy 188 ASPSTIISVSVFIVPIIVIAICYSVFCARROHALLVNWKRHSLEVRKDCVENDE 247

Db 180 EEPGVLFSAIGSEFYLPLAILVMYCRVYVAKR-----ESRGL 218

Qy 248 EGAERKEFEODESERRRQHEBEVAKEREMAKOSLKAEGSTGTSSEVARGSEYVR 307

Db 219 KSGKLTGDSDEQYTLRIHRNAPR-----GGSGMASAKTKTHFSVPL- 261

Qy 308 ESSVVASDGSMEGEGSTKVEENSMKADKGRTEVNOCSIDIGEDMGEEDINSEDDV 367

Db 262 -----LFSRER- 268

Qy 368 EAVNIPESLPPSRNSNPPLPRCOCRAKAVIFIIIFSVLSLGPYCFGLAVLAWVDV 427

Db 269 -----KAKTLGIVGCFVLCWLPF-FLVMPIGSFPF 299

Qy 428 ETQVPMYITIIIMLFLOCCIHPIYVGYGMHTIKKEIODMLK-KFCKEKPKPE----D 482

Db 300 DKFSEIVFKIVFMWGLNSCINPIYPCSSQEFKAPQNVLRIOCLCRKOSRHALGYT 359

Qy 483 SHPLPGTEGGTEGKI-VPSYDSATF 507

Db 360 LHPSQAVEGQHKDMVRIPVGSRETF 385

RESULT 15

US-08-228-932-6

Sequence 6, Application US/08228932

Patent No. 5578611

GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,

APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig

TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN

TITLE OF INVENTION: PROSTATIC HYPERPLASIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/228,932

FILING DATE: 13-APR-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41878-B/JPM/TEP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: (212) 422523 COOP UI

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 466 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-228-932-6

Query Match 12.8%; Score 338.5; DB 1; Length 466;

Best Local Similarity 21.3%; Pred. No. 1.2e-19;

Matches 108; Conservative 80; Mismatches 187; Indels 131; Gaps 11;

Qy 8 STRESNSHRCMPKSPKIPSLAHGIIRSTVIVIFLAASFGVNIYALVLOKRPOLQVYN 67

Db 5 SGNASDSSNCRP--PAVNISSKAILLGVILGILFVGLNIIYILSVACHRHLSVTH 62

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0y      68  REFILLTDLQSLVAPWVAVASVPLPMAHNSHCTALVSLTHLFAFASVMTVIVSV  127
Db      63  YIYNLAVADLLLTSTVLPESAIEVGLGMAFGVFCNMAVADVLCCTASIMGLCTISI  1222
Qy      128  DRYIYIHPILSYPSKMTQRRGYLLLTGTVIAVLIQSTPPLRYGWAQAFDERNALCSMIWG  1877
Db      123  DRYIGVSPLRPRTVITVTRGRILMILLCVMASTLVSIGLPFGMRQPA - PEDETICOI - N  179
Qy      188  ASPSTIISVVSFYIPIPLVIMVACYSVFCARQROHLLVVKRHSLEVAVKVCVENEDE  2477
Db      180  BEPGVILFSAIGSFYLPALITLVMICRYVYAKR-----BSRGL  218
Qy      248  EGAEEKKEEFODESEFRROHEEVEVAKEGRMKAGSLKAKEGSTGTSESSVEARGSEVR  3077
Db      219  KSGLKTRKSDSEQYTLRIHRKNPA-----GSGGMSASATKTHFSVRL-  261
Qy      308  ESSIYVASDGSMEKGEGSTKVEENSMKADKGTENVQCSIDLGEDDMFEGEDDINFSEDDV  3677
Db      262  -----LKFSREK-  268
Qy      368  EAVNIPESLPSRNSNSNPPLPRCYOCKAKAVFIIFISVSLTSGPYCFVLAVLAVADV  4277
Db      269  -----KAKTIGIYVGCFCVLQWLPF -FLVMP IGSEFP  2999
Qy      428  ETQVQWVITIIIMVLFLOCCIHRYVYGVMHTIKETIDMK -KFECKEKPRKE----D  4822
Db      300  DKFPSEYFKEIVFMVGLYNSCINPIFYPCSQSEFKKAFQVNLRIQCLCRGROSSKHALGYT  3599
Qy      483  SHPDLPRTEGEGTEGI -VPYSDATSF  507
Db      360  LHPPSQAVEGQHKKDMVRLIPVSGREF  385

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Search completed: October 28, 2002, 16:47:28  
Job time : 19 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:44:33 ; Search time 21 Seconds  
(without alignments)  
2324.447 Million cell updates/sec

Title: US-09-992-238-2

Perfect score: 2644

Sequence: 1 MTSCTNSTRESNSSHTCMP.....GTGGTGKIVPSYDSATRP 508

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR71:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343.5	13.0	490	2 A35546	muscarinic acetylcholine receptor M4 - chicken
2	340.5	12.9	422	2 I38209	serotonin receptor
3	340	12.9	477	2 S71323	alpha-1A adrenergic
4	336	12.7	466	2 I57959	alpha-1C adrenergic
5	335.5	12.7	421	2 I49375	serotonin receptor
6	333.5	12.6	429	2 S65656	alpha-1C-adrenergic
7	333.5	12.6	466	2 JN0765	alpha-1C-adrenergic
8	333.5	12.6	499	2 S65657	alpha-1C-adrenergic
9	331.5	12.5	422	2 JH0315	serotonin receptor
10	325.5	12.3	466	2 A35375	alpha-1-adrenergic
11	319	12.1	509	2 A47174	serotonin receptor
12	314.5	11.9	501	2 JH0447	alpha-1A-adrenergic
13	314.5	11.9	572	2 I39369	alpha-1A-adrenergic
14	312.5	11.8	484	2 S48657	muscarinic acetylcholine receptor
15	306.5	11.6	560	2 A38731	muscarinic acetylcholine receptor
16	304.5	11.5	601	2 JH0170	octopamine receptor
17	296.5	11.2	601	2 S12004	tyramine receptor
18	294	11.1	466	2 S10856	muscarinic acetylcholine receptor
19	291	11.0	466	2 JH0197	muscarinic acetylcholine receptor
20	291	11.0	479	2 S10127	muscarinic acetylcholine receptor
21	289	10.9	466	2 A27386	muscarinic acetylcholine receptor
22	288	10.9	488	2 T15941	hypothetical protein
23	288	10.9	515	2 JCI525	alpha-1B-adrenergic
24	287	10.9	466	2 S10126	muscarinic acetylcholine receptor
25	285	10.8	610	2 T32917	hypothetical protein
26	283	10.7	515	2 A40491	alpha-1-adrenergic
27	283	10.7	517	2 A45121	alpha-1B-adrenergic
28	282.5	10.7	478	2 C29514	muscarinic acetylcholine receptor
29	282	10.7	479	2 S33776	muscarinic acetylcholine receptor

30	280	10.6	466	2 A40972	muscarinic acetylcholine receptor
31	279.5	10.6	476	2 JC5042	G protein-coupled
32	277.5	10.5	531	2 JT0531	muscarinic acetylcholine receptor
33	276	10.4	564	2 A38271	serotonin receptor
34	275.5	10.4	484	2 S58868	G protein-coupled
35	275.5	10.4	532	2 JT0530	muscarinic acetylcholine receptor
36	273	10.3	443	1 DYH02	dopamine receptor
37	273	10.3	445	2 A48881	serotonin receptor
38	270	10.2	448	2 A47519	serotonin receptor
39	268	10.1	448	2 S36402	serotonin receptor
40	267.5	10.1	442	1 DYXLD2	dopamine receptor
41	265	10.0	501	2 T18863	hypothetical protein
42	262.5	9.9	445	2 T42203	serotonin receptor
43	260	9.8	430	2 T16079	hypothetical protein
44	259.5	9.8	589	2 B29514	hypothetical protein
45	258	9.8	460	2 A31897	muscarinic acetylcholine receptor

ALIGNMENTS

RESULT 1

A35546 muscarinic acetylcholine receptor M4 - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 21-Jul-2000  
C:Accession: A35546  
R:Titelje, K.M.; Goldman, P.S.; Nathanson, N.M.  
J. Biol. Chem. 265, 2828-2834, 1990  
A:Title: Cloning and functional analysis of a gene encoding a novel muscarinic acetylcholine receptor  
A:Reference number: A35546; MUID:90153912  
A:Accession: A35546  
A:Molecule type: DNA  
A:Residues: 1-490 <TIE>  
A:Cross-references: GB:J05218; NID:g211067; PIDN:AAA48563.1; PID:g211068  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein; status predicted <TM1>  
F:42-67/Domain: transmembrane #status predicted <TM1>  
F:80-104/Domain: transmembrane #status predicted <TM2>  
F:117-138/Domain: transmembrane #status predicted <TM3>  
F:158-181/Domain: transmembrane #status predicted <TM4>  
F:203-226/Domain: transmembrane #status predicted <TM5>  
F:413-433/Domain: transmembrane #status predicted <TM6>  
F:445-466/Domain: transmembrane #status predicted <TM7>

Query Match 13.0%; Score 343.5; DB 2; Length 490;  
Best Local Similarity 23.7%; Pred. No. 8.2e-16;  
Matches 116; Conservative 94; Mismatches 176; Indels 103; Gaps 17;

QY	36	TVLVIFLA-----	ASFGNIYALVLRKPKQLQVTFNFIHLVTDL-----	QISL 83
DB	39	TVELVFATVYTGSLVTVVGNLILMLSIKYNRLQVNNYFLSLACADILIGVFSMNL		98
QY	84	VAPVAVATVSVLPFPLNSHFTALVSLTFLPAFASVTIVTVSVDRSLIHPSPYSKM		143
DB	99	YTVYIILG----YMPGLAVVCDLWLDLDYVSNVSNMILLISDRFCVYKPLTFYARR		154
QY	144	TQRCGYLLVGTWITVAIILOSTPPLYGW---GQAAPFERNALCSMIGASPSYTIILSVS		199
DB	155	TTKAGLMIAAAWILSLFLMAPAILFMQFIYGRKTRHERE--CYIQFLSNPAVFGTAIA		212
QY	200	FIVPLVIMACYSVVCAARQHALLVNKRHSLEPR-----	YKDEVN 244	
DB	213	AFVPLVIMVLYLHIISLASHR-----VRRHPRSKRERKSKLSFFKAPVKKNNN		266
QY	245	EDEGAKEKEEFODESEFRROHEGEVAKKGRMAKGSILKAKGSTGTSSEVARGSE		304
DB	267	SPKAAVEKEEYRN-----GKV-----DDPSAQDEAIGQDEE-----	KE 301	
QY	305	EVRSSTVASDGSMEGRGSTRVENSMAKADGRTEVNGCSIDIGEDMERGEDINFESE		364
DB	302	TSNDSSTVSMQTQTKRKP-TTEILPAGOGGSPAPRVPPTS-----KMSKIKIYTKQ		352

Qy	365	DDVEVNINPELSLP----	PSRRN--SNSNP-LPRCY-----	QCKAAKY	400
Db	353	TGTETVTAIEIVPAKAGASDHNSLSNPANVAKFASIRSOYRKRRQMAAREKKATRT			412
Qy	401	IFIIFFSVLSGPGCFGLAVLVAVWDVETQVQWVITIIIMFLQCCIHPRUYUGVNHKT			460
Db	413	IFAILLAIVLTWPIYVNVAVLNTF--CETCVPELVMSIGVLCYVNSTINPACTALCMAT			470
Qy	461	IKKEIQDML	469		
Db	471	EKKTFKHL	479		

RESULT 2  
138200

serotonin receptor 1A - human  
N.Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)  
C.Species: Homo sapiens (man)  
C.Date: 06-Sep-1996 #sequence, revision 15-May-1998 #text\_change 21-Jul-2000  
C.Accession: I38209, I37104; S07343; I56176; S31438  
C.Jacobson, J.S.; Refolo, L.M.; Conley, M.P.; Sambamurti, K.; Humayun, M.Z.  
C.utat. Res. 179, 89-101, 1987  
A.Title: DNA replication-blocking properties of adducts formed by aflatoxin B1-2,3-dichloroacetate  
A.Reference number: I38209; MUID:87258013  
A.Accession: I38209  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-422 <JAC>  
A:Cross-references: EMBL:X57829; NID:g36428; PIDN:CAA040962.1; PID:g36429  
R.Parks, C.L.; Chang, L.S.; Shenk, T.  
Nucleic Acids Res. 19, 7155-7160, 1991  
A>Title: A polymerase chain reaction mediated by a single primer: cloning of genomic sequences  
A.Reference number: I37104; MUID:92115564  
A.Accession: I37104  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-9 <PAR>  
A:Cross-references: EMBL:Z11168; NID:g1033027; PIDN:CAA77560.1; PID:g1033028  
R.Koblick, B.K.; Fritelle, T.; Collins, S.; Yang-Feng, T.; Koblicka, T.S.; Francke, U.; Le  
Nature 339, 75-79, 1987  
A>Title: An intronless gene encoding a potential member of the family of receptors coupled  
A.Reference number: S07343; MUID:87315369  
A.Accession: S07343  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-151, 'PR', 155-171, 'I', 173-417, 'N', 419-422 <KOB>  
A:Cross-references: EMBL:X13556; NID:g35523; PIDN:CAA31908.1; PID:g35524  
A>Note: the authors translated the codon ATC for residue 172 as Met  
R.Aune, T.M.; McGrath, K.M.; Sarr, T.; Bombara, M.P.; Kelley, K.A.  
J. Immunol. 151, 1175-1183, 1993  
A>Title: Expression of 5HT1A receptors on activated human T cells. Regulation of cyclic  
A.Reference number: I56176; MUID:93329096  
A.Accession: I56176  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 'RPR', 203-227, 'R', 229-244, 'A', 245-354, 'T', 356-362, 'MRP' <AUN>  
A:Cross-references: GB:S64045; NID:g404416; PIDN:AAD13945.1; PID:g4261645  
C.Genetics:  
A:Gene: HTR1A; ADRB2RL1; ADRBR1L  
A:Cross-references: GDB:120686; OMIM:109760  
A:Map position: 5cen-5q11  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter receptor  
F.37-62/Domain: transmembrane #status predicted <TM1>  
F.74-98/Domain: transmembrane #status predicted <TM2>  
F.110-113/Domain: transmembrane #status predicted <TM3>  
F.115-178/Domain: transmembrane #status predicted <TM4>  
F.192-211/Domain: transmembrane #status predicted <TM5>  
F.346-367/Domain: transmembrane #status predicted <TM6>  
F.379-403/Domain: transmembrane #status predicted <TM7>  
F.10, 11, 24/Binding site: carbohydrate (Asn) #status predicted  
F.109-187/Disulfide bonds: #status predicted  
F.420/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match	12.9%	Score 340.5;	DB 2;	Length 422;
Best Local Similarity	22.0%;	Pred. No. 1.1e-15;		
Matches 101; Conservative	92;	Mismatches 190;	Indels 77;	Gaps 9

QY	26	ISLHGIIRSVLIVLFIPLASFGVN--IYLVLIORKPOLLQVTRNRFNMLVLTLLISL	83
Db	31	VTVSGVITISLLGLTGLIFCVALGNACVVAALALER--SLQVNAVYLLIGSLAVTDLAMSVL	88
QY	84	VAPVNVATSVPLEMPNLNSHFTALVSLTHLFPASVNTIVLVSVDYRLSIHTPLSYSKM	143
Db	89	VLPMAALQVILNKTKTTLGQVTDLLFIADLVLCSTSIHLCAIALDRYVAITDPIDYVNR	148
QY	144	TQRBGYLLVGTWIVLAILOSTPRPLYGMGGAARFDEBNALCSIMWASPSYTLTVSVSFTVI	203
Db	149	TPRRRAALISLTWLLGLFISTIPRMIGMTRP--EDRSDDACTISKDGHGTYTISFGAFYI	206
QY	204	PLIVAIACYSVVFCARORHALLNVKRRHSLVRYKDCVENEDEGAERKEEFODESEFR	263
Db	207	PLLLMLVLYGRIFRANR-----FRIKRTVKKVEKTAGDTRHGASPARQPK	251
QY	264	ROHEVEYNAKACGRM--EAKDGL-----KAKDGSITGISESSVEARGSELEVAESSTVASDG	316
Db	252	KSVNGESSSRMWRIGVESKAGGALCANGAVRQGDGALLEVYH-----	296
QY	317	SMECKEGSTKVEENSMKADKGRTEVNOCSIDLEGDMFEGDDINFSDDVEAVNIPESL	376
Db	297	----RVGNRSK-EHLPLPSEAGPTPCAPASFE-----	322
QY	377	PPSRNSNSNPPLPRCYOCKAKAAYIIIIISFVYLSLGRPYCLAVLAVWVDYETOPQWVI	436
Db	323	RKNENNAEAKRKMALABERKTVKTLGIIMGFFIILCMLPEFFIVALVLPDCESSCHMPTLLG	382
QY	437	TIITLIFLQCCIHPIYVYGVMMHTIKKEIOMLKKPFCKE	476
Db	383	AIITNWLGSNLSLNEVLIATYFNKDFQNAFKYTIKKKPCFQ	422

## RESULTS

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alpha-1A adrenoergic receptor - Japanese medaka
C:Species: Oryzias latipes (Japanese medaka)
C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C:Accession: S71323
R:Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 235, 501-507, 1996
A:Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of
A:Reference number: S71323; MUID:96184522
A:Accession: S71323
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-477 <YAS>
A:Cross-references: EMBL:D63859
A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
C:Superfamily: vertebrate rhodopsin

Query March 12.9%; Score 340; DB 2; Length 477;
Best Local Similarity 23.8%; Pred. No. 1,4e-15;
Matches 119; Conservative 66; Mismatches 160; Indels 134; Gaps 14;

QY 12 SSSHTTCMPLSKMPISLAHGIRSTVLVTFPAASFVGNIVLALVLQRRPOLLOVYTNREIF 71
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Db 18 SNCSHVLAP----ELNTGKAVVLGVLGIFLFGVIGNIVLVSVCRRHLOTVTYTYPI 73

QY 72 NLLVTDLLQISLVAPMWVAVTSVPLFMPLNSHPCRALVSLTHLFAFASNTIVLSVDRYL 131
    |||| : : : : : |||| : : : : : |||| :
Db 74 NLAAVDLLLSSTVLPFESAIFELDRWVEGRVFCNIMAADVLCCTASIMSLCVISVDRIYI 133

QY 132 SIHLSPYSKMTQRRGLLYGTWIVAIIQSTPLNSGVGOAEDERNALCSMTMGASPIS 191
    :||| : : : : : : : : : : : : : : : : : : :
Db 134 GVSYPLRPLALMTKRALLAVMLLVLSVIISIGLFGMKRPA-PEDETVCKIT--EEPG 190

QY 192 YTIISVSEFIVPLIVMTACTSVVFCARROHALLINVKRSLSLEVRYKDCVENEDEGAE 251

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Db 191 YAIRSAAGSYFLPLAIIILAMWCGRYVAAQKESRGL-----KEG-Q 229
QY 252 KKEPFODESEFRROHEGEYKAKEGRMEAKDGSLKAKEGSTGTSSSEVARGSEVRESST 311
Db 230 KIEKSDSEQVILFRMRG-----NTT 249
QY 312 VASDGSMEKGEKSTKVEENSMKADKGRTEVNOCSIDGEDDMEGEDDINFSEDDVEAVN 371
Db 250 VSED-----EALRSRT-----HFALRLKFSREK----- 273
QY 372 IPESLPSSRRNSNPNPLPRCYOCKAKAVIFIIIFSYVLISGYPCLAVLAWVDVEYOV 431
Db 274 -----KAKTLGIIVGCEVLCMLP--FLVLPDGSIFPAPR 307
QY 432 P-QWVITIIWLFELCCIHPIYGYVMHKITKEIQDMLKKFKCEKPKEDSHPDLPGT 490
Db 308 PSDIVFKITFWLGFNSCINPIIILCSNOEFKKAFOSLT--GVHCLRMTPRAHHH--HLSVG 365
QY 491 EGGTEG-KIIVSYDSATFP 508
Db 366 QSOTGHSITITLSDSKAP 384

```

## RESULT 4

157959

alpha-1C adrenergic receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Apr-2000

C:Accession: I57959; I52862; PC2179

R:Laz, T.M.; Forray, C.; Smith, K.E.; Bard, J.A.; Vayase, P.J.; Branchek, T.A.; Weisshar

Mol. Pharmacol. 46, 414-422, 1994

A&gt;Title: The rat homologue of the bovine alpha 1c-adrenergic receptor shows the pharmac

A:Reference number: I57959; MUID:95021119

A:Accession: I57959

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-466 &lt;RES&gt;

A:Cross-references: EMBL:U07126; NID:g595275; PIDN:AAA62866.1; PID:g595276

R:Stewart, A.F.; Rokosh, D.G.; Bailey, B.A.; Karns, L.R.; Chang, K.C.; Long, C.S.; Karly

Circ. Res. 75, 796-802, 1994

A&gt;Title: Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. alpha 1C

A:Reference number: I52862; MUID:95008062

A:Accession: I52862

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-38, 'L', 40-66, 'G', 68-466 &lt;RE2&gt;

A:Cross-references: EMBL:U13368; NID:g555851; PIDN:AAA52103.1; PID:g555852

R:Rokosh, D.G.; Bailey, B.A.; Stewart, A.F.R.; Karns, L.R.; Long, C.S.; Simpson, P.C.

Biochem. Biophys. Res. Commun. 200, 1177-1184, 1994

A&gt;Title: Distribution of alpha 1C-adrenergic receptor mRNA in adult rat tissues by RNase

A:Reference number: PC2179; MUID:94241969

A:Accession: PC2179

A:Molecule type: mRNA

A:Residues: 102-279 &lt;ROK&gt;

A:Experimental source: cardiac myocyte

C:Comment: This factor comprises a multigene family. As do alpha-2 and beta-adrenergic r

C:Superfamily: vertebrate rhodopsin

C:Keywords: neurotransmitter receptor; transmembrane protein

F:26-42/Domain: transmembrane #status predicted &lt;TM1&gt;

F:73-89/Domain: transmembrane #status predicted &lt;TM2&gt;

F:104-120/Domain: transmembrane #status predicted &lt;TM3&gt;

F:147-163/Domain: transmembrane #status predicted &lt;TM4&gt;

F:195-211/Domain: transmembrane #status predicted &lt;TM5&gt;

F:276-292/Domain: transmembrane #status predicted &lt;TM6&gt;

F:306-329/Domain: transmembrane #status predicted &lt;TM7&gt;

```

Db 7 NASEGSMCTH-----PPAPVNIKAILLGVILGGLIFGVNLITVILSVACHRHLSVT 61
QY 67 NRIIFNLVLDLQISLVAPEVAVTSPFLPPLNSHCTALVSLTHLPARASVTIYLV 126
Db 62 HYIYVNLAVADLLTSTVLPESAIFELIGVAFGRVCNMAAADVLCCTASINGLITIS 121
QY 127 VDRITSIHPLSYPSKMTORRGVLLYGTWIVALLQSPPLYGWGOAFDRNALCMTW 186
Db 122 IDRIIGVSYPLRPTIYTORRGVALLCWVLSIVISIGLPGKRPDA--PEDETICQI-- 178
QY 187 GASPTYTLVSVSPFIVPLIYMIACYSVFCARROHALLYVNRHSLVVRKDCVENED 246
Db 179 NEERGVLVFSALSGFYPVLAIIIMWCGRYVAVR-----ESRG 217
QY 247 EEGAEKKEEFDSEFRROHEGEYKAKEGRMEAKDGSLKAKEGSTGTSSSEVARGSEV 306
Db 218 LKSLGKTDKSDSEQVTLRIHRKNVPAEG-----GVSSA----- 251
QY 307 RESSTVASDGSMEKGEKSTKVEENSMKADKGRTEVNOCSIDGEDDMEGEDDINFSEDD 366
Db 252 -----KNT-----HFSVRLKFSREK 268
QY 367 VEAVNIPESEPPSSRRNSNPNPLPRCYOCKAKAVIFIIIFSYVLISGYPCLAVLAWVD 426
Db 269 -----KAKTLGIIVGCEVLCMLP--FLVLPDGSIFPAPR 298
QY 427 VETQVPOWVITIIWLFELCCIHPIYGYVMHKITKEIQDMLKKFKCEKPKEDS--- 483
Db 299 PDFPSEVFEKIVFWLGYLNSCINPIIILPCSSOEFKKAFOVLRIOCLRRROSSKHALGY 358
QY 484 --HPDLEGTGTEGKI--VPSYDSATFP 507
Db 359 TLHPPSQALBEGQHRDWMVRIPIVSGETP 385

```

## RESULT 5

149375

serotonin receptor 1A - mouse

N:Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A).

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999

C:Accession: I49375; A57508

R:Charost, A.; Wainer, B.H.; Albert, P.R.

J. Neurosci. 13, 5164-5171, 1993

A&gt;Title: Cloning and differentiation-induced expression of a murine serotonin1A recep

A:Reference number: I49375; MUID:94076019

A:Accession: I49375

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-421 &lt;CHA&gt;

A:Cross-references: EMBL:U39391; NID:g1066325; PIDN:AAA81519.1; PID:g1066326

R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, G

Genomics 18, 175-184, 1993

A&gt;Title: Identification, chromosomal location, and genome organization of mammalian G

A:Reference number: A48909; MUID:94116980

A:Accession: A57508

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 136-176, 'T', 178-241, 'L', 243-246, 'V', 248-262, 'W', 264-303, 'H', 305-329, 'I', 3

A:Cross-references: GB:L20339

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran

F:37-62/Domain: transmembrane #status predicted &lt;TM1&gt;

F:74-98/Domain: transmembrane #status predicted &lt;TM2&gt;

F:110-132/Domain: transmembrane #status predicted &lt;TM3&gt;

F:153-178/Domain: transmembrane #status predicted &lt;TM4&gt;

F:192-217/Domain: transmembrane #status predicted &lt;TM5&gt;

F:346-367/Domain: transmembrane #status predicted &lt;TM6&gt;

F:379-403/Domain: transmembrane #status predicted &lt;TM7&gt;

F:109-187/Disulfide bonds: #status predicted

```

Query Match 12.7%; Score 336; DB 2; Length 466;
Best Local Similarity 21.3%; Pred. No. 2.3e-15;
Matches 108; Conservative 79; Mismatches 186; Indels 134; Gaps 11;

```

```

QY 7 NSTRENSNHFCTMKPDLKMPISLAGIIRSYLVIFLASFGNIVLVLQRRKPOLLOVY 66

```

Best Local Similarity 23.2%; Pred. No. 2,4e-15;  
Matches 106; Conservative 88; Mismatches 190; Indels 73; Gaps 12;

QY 26 ISLAHGIIRSVLVIPLFLASFVGN--IVLALVLRKQQLQVTRFIFNLITDLOISL 83  
Db 31 VTSYVYITSLTGLTFLFCALNACVVAIAIER--SLOWNAVYLLGSLAVLWLVSVL 88  
QY 84 VAPVAVTSVPLEPPLNSHCTALVSLTHLFAFASVNTIVLVSDRYLSIIHPLSPSKM 143  
Db 89 VLPMAALYQVNLKNTLQOVCDLFIADVLQCTSSILHLCAIALDRWATIDPIDYNNKR 148  
QY 144 TORRGVLLYGTWIVAILQSTPPLYGQQAIFDERNA-LCSMTIGASPSYITLSVSEFIV 202  
Db 149 TPRRAAALISLTWILGFLISIPMLGW-RAPEDRSNPECTI--SKDHGYITSTFGAFY 205  
QY 203 IPLIVMAYCSVFCARQRRHALLYNKRSLERVKDCVENEDEGAKEKEEQDSEF 262  
Db 206 IPLILMLVYLGRIFRAR-----FRINKYAKKVKGA----- 238  
QY 263 RROHEGEVAKKEGMEAKDGLAKEGSTGTSSESVARGSEVEEVSSTVADSGM-EGK 321  
Db 239 -----GTSFGTSSAPPKKSLNG-QPGSGDCRSRAEMRAVGTPCANCAVRQGE 285  
QY 322 EGST--KVENSKMAKDKGRTEVNQCSIDLGEDMEFGEDDINSEDDVEAVNIPESLP-P 378  
Db 286 DDATLEVEIEVHRVGNKSG-----DLPLPSESGANSVYPACLERK 324  
QY 379 SRRNSNSNPPLPRCYOCCAKAVFIIFISVYLSLGPYCLAVLAVWVDEVOVQWVITI 438  
Db 325 NERFAEKRRKMAALAREKRYKTLGITLGLTFLCMLPFIYALVLPCESSCHMBELLGAI 384  
QY 439 IIMLFLOCCIHPIYVGYMHTIKETIDMLKFFCK 475  
Db 385 IIMLGYSNLSLNPYIYAVFNKDFQNAFKTIKCFKR 421

RESULT 6  
S65656  
alpha-1C-adrenergic receptor splice form 3 - human

N:Alternate names: alpha-1C-adrenoceptor isoform 3  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 20-Jun-2000  
C:Accession: S65656; S65654  
R:Tanaka, T.  
Submitted to the EMBL Data Library, July 1994  
A:Reference number: S65656  
A:Accession: S65656  
A:Molecule type: mRNA  
A:Residues: 1-429 <TAN>  
A:Cross-references: EMBL:D32201; NID:9927210; PIDN:BA06900.1; PID:9927211  
R:Hirasawa, A.; Shibata, K.; Horie, K.; Takel, Y.; Obika, K.; Tanaka, T.; Muramoto, N.;  
FEBS Lett. 363, 256-260, 1995  
A:Title: Cloning, functional expression and tissue distribution of human alpha(1C)-adren  
A:Reference number: S65654; MUID:95255557  
A:Molecule type: mRNA  
A:Accession: S65654  
A:Residues: 424-429 <HIR>  
A:Cross-references: EMBL:D32201  
C:Genetics:  
A:Gene: GDB:ADRA1C; ADRA11  
A:Cross-references: GDB:I28088; OMIM:104221  
A:Map position: 8p21-8p11.2  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 12.6%; Score 333.5; DB 2; Length 429;  
Best Local Similarity 21.1%; Pred. No. 3.3e-15;  
Matches 107; Conservative 79; Mismatches 189; Indels 131; Gaps 10;

QY 8 STRESNSHHCMPISKMPISLAHGIIRSVLVIPLFLASFVGNIVLALVLRKQQLQVTRF 67  
Db 5 SGNSSDSSNCTQP--PAPVAVTSVPLEPPLNSHCTALVSLTHLFAFASVNTIVLVSDRYLSIIHPLSPSKM 62

QY 68 RFIENLITDLOISLAVPWWVATVPLEPPLNSHCTALVSLTHLFAFASVNTIVLVSV 127  
Db 63 YVIVNLAVADLLITSLTVLPFAIPEVLGVNAFGVFNINMAAVDVLCTASIMGLCIISI 122  
QY 128 DRYISIIHPLSPSKMQRGQYLLYGTWIVAILQSTPPLYGQQAIFDERNALCSMTIG 187  
Db 123 DRYIGSVYPLRYPIVIVQRLMALLCVMAISLVSIGPLFGWRQPA-PEDETICQI--N 179  
QY 188 ASPSTILSVSFEIPLIYMAICYSVFCARQRRHALLYNKRSLERVKDCVENEDE 247  
Db 180 EEPGYVLFSAIGSYLFLAILIIVMYCRYVYAKR-----ESRGL 218  
QY 248 EGAKEKEEPODESEFRROHGEVAKKEGMEAKDGLAKEGSTGTSSESVARGSEVEVR 307  
Db 219 KSGLKTDKSDSEQVTLIRHKNAPA-----GSGMSAKTKTHFVRL- 261  
QY 308 ESSIVASDGSMEKEGEGTKVEENSKMDKGRTEVNQCSIDLGEDMEFGEDDINSEDDV 367  
Db 262 -----LKFSEK- 268  
QY 368 EAVNIPESLPSRRNSNSNPPLPRCYOCCAKAVFIIFISVYLSLGPYCLAVLAVWV 427  
Db 269 -----KAKTIGIVGCVLCMLPF-FLVMPIGSEFP 299  
QY 428 ETQYQWVITIIIMLFLOCCIHPIYVGYMHTIKETIDMLKFFCKEKPREDSE--- 483  
Db 300 DFKSETFVETIVFWLGLNSCINPIIYPCSSQEFKKAQVNLRIQCLRRQSSKHALGYT 359  
QY 484 -HPLPTEGTECKEIT-VPSYDSATF 507  
Db 360 LHPPSAVEGOHKDMVRIPVGSRETF 385

RESULT 7  
JN0765

alpha-1C-adrenergic receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 21-Jul-2000  
C:Accession: JN0765; I84635; J02333; G01419  
R:Hirasawa, A.; Horie, K.; Tanaka, T.; Takagaki, K.; Mural, M.; Yano, J.; Tsujimoto,  
Biochem. Biophys. Res. Commun. 195, 902-909, 1993  
A:Title: Cloning, functional expression and tissue distribution of human cDNA for the  
A:Reference number: JN0765; MUID:93384619  
A:Accession: JN0765  
A:Molecule type: mRNA  
A:Residues: 1-466 <HIR>  
A:Cross-references: GB:L31774; NID:9666892; PIDN:AAB59486.1; PID:9666893  
R:Diehl, N.L.; Shreeve, S.M.  
Eur. J. Pharmacol. 268, 393-398, 1994  
A:Title: Identification of the alpha 1C-adrenoceptor in rabbit arteries and the human  
A:Reference number: I47013; MUID:95104335  
A:Accession: I84635  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 202-344 <DIE>  
A:Cross-references: GB:S76001; NID:9913817; PIDN:AAD14205.1; PID:94261905  
R:Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D  
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994  
A:Title: Cloning, expression and characterization of human alpha adrenergic receptors  
A:Reference number: J02331; MUID:94296402  
A:Accession: J02333  
A:Molecule type: mRNA  
A:Residues: 1-130, 'F', 132-140, 'P', 142-166, 'C', 168-247, 'H', 249-337, 'C', 339-430, 'Q', 432  
A:Cross-references: GB:S70782; NID:9547219; PIDN:AAB31163.1; PID:9547220  
R:Elliston, K.O.  
Submitted to the EMBL Data Library, April 1994  
A:Reference number: G06938  
A:Accession: G01419  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 296-346, 'C', 348-430, 'Q', 432-466 <ELL>  
A:Cross-references: EMBL:U08994; NID:9497243; PIDN:AAA18783.1; PID:9497244  
C:Comment: This protein plays critical roles in the regulation of a variety of physio

C:Genetics:  
A:Gene: GDB:A08ALC; ADRALI  
A:Cross-references: GDB:I28088; OMTM:104221  
A:Map position: 8p21-8p11.2  
A:Introns: 295/3  
A>Note: The list of introns may be incomplete  
C:Superfamily: vertebrate rhodopsin  
F:26-51/Domain: alternative splicing; glycoprotein; receptor; transmembrane protein  
F:66-90/Domain: transmembrane #status predicted <TM1>  
F:101-122/Domain: transmembrane #status predicted <TM2>  
F:144-165/Domain: transmembrane #status predicted <TM3>  
F:183-205/Domain: transmembrane #status predicted <TM4>  
F:274-298/Domain: transmembrane #status predicted <TM5>  
F:306-329/Domain: transmembrane #status predicted <TM6>  
F:7.13/.22/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 333.5; DB 2; Length 466;  
Best Local Similarity 21.1%; Pred No. 3.7e-15;  
Matches 107; Conservative 79; Mismatches 189; Indels 131; Gaps 10;

OY 8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAAEFNGNVLAVLRQKPOLQVTN 67  
Db 1 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
5 SGMASSDSCNCQP--PAPVNISKAILLGVLIGLLIFGLGNILVLVSACRHHLSVTH 62  
OY 68 REFNULTVDLQLQISLVARVVVATSVPLEFWPLNSHFCTALVSLTLFAFASVNTIVLVSY 127  
Db 63 YIIVMLAADLLLTSTVPFPFSAFIEFLGVMARGVFNCITMAADVLCCTASINGLICIIISI 122  
OY 128 DRYLIHLPLSYAMTORGYLLTGTWIVAIILOSTPPLYXMGGAFFERNALGSMING 187  
Db 123 DRVIVSIPLRPIPTVYTORRGIMALLCVALLSVISIGLPFGWRQPA-PEDETTCOI--N 179  
OY 188 ASPSYTIISVSVFIYPIVLVIACYSVVEFCARRQHALLNYNRHSLEVRVKDCVENEDE 247  
Db 180 EEPGVYLFPSALGSFYPLAIIILVMCRVYVAKR-----ESRGL 218  
OY 248 EGAEKEKEPFODESEFRROHEGEVKAKEGRMEAKDGSLAKEGSTGTSSESVEARSGEEVR 307  
Db 219 KSGLTIDKSDSQVTLRLHRKNAPA-----GGSGMASAKTKTFHFVRL- 261  
OY 308 ESSYAAGDSMGCKGSGSTVEENSMKADKGTEVNCQSIDLGDDIMEFGEDDIINFSEDDV 367  
Db 262 -----LKFSREK- 268  
OY 368 EAVINPESLPPSRNSNSNPPLRCYCOKAKAVIFIIFSYYLSLGPYCLAVLAWVDV 427  
Db 269 -----KAAKTIGIVGCCFVLCMLPF-FLVWPDISFFP 239  
OY 428 ETVOQWMVITIIWLFLFOCCIHPYVYGVMHKTIKKEIDMLKKFFCKEKPPEKDS--- 483  
Db 300 DFKPSSETFEFKIIFYWGVLNSCINPLIYPCCSOEFKKAFOINVLRIOCLRROSSKHALGYT 359  
OY 484 -HPDLPGTEGEGTEGKI-VPSYDSATE 507  
Db 360 LHPPSQAVEGQHDKDMVRIIPVGSRETF 385

RESULT 8  
S65657  
alpha-1C-adrenergic receptor splice form 2 - human  
N:Alternate names: alpha-1C-adrenoceptor isoform 2  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 20-Jun-2000  
C:Accession: S65657; S65655  
R:Tanaka, T.  
submitted to the EMBL Data Library, July 1994  
A:Reference number: S65656  
A:Accession: S65657  
A:Molecule type: mRNA  
A:Residues: 1-499 <TAN>  
A:Cross-references: EMBL:D32202; NID:g927208; PIDN:BA06901.1; PID:g927209  
R:Hirasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Odika, K.; Tanaka, T.; Muramoto, N.;

FEBS Lett. 363:256-260, 1995

A>Title: Cloning, functional expression and tissue distribution of human alpha(1C)-ad  
A:Reference number: S65654; MUID:9525557

A:Accession: S65655

A:Molecule type: mRNA

A:Residues: 424-499 <HIR>

A:Cross-references: EMBL:D32202

C:Genetics:

A:Gene: GDB:ADRA1C; ADRA1L1

A:Cross-references: GDB:I28088; OMIM:104221

A:Map position: 8p21-8p11.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 12.6%; Score 333.5; DB 2; Length 499;  
Best Local Similarity 21.1%; Pred. No. 4e-15;  
Matches 107; Conservative 79; Mismatches 189; Indels 131; Gaps 10;

OY 8 STRENSHTCMPLSKMPTSLAHGILRSTVLYFLASFGVGNVALVLQKKPQLLOYTN 67  
| : |||| : | : || : : : : |||| : | : || :  
Db 5 SGNAADSSNCTOP--PAVINISKALLGLVLLGGILLFCVNLITLVLSACHRLHSYTH 62  
| : |||| : | : || : : : : |||| : | : || :  
OY RFIPIILWTDLDLOISLVAPWAVATVPLEFWPLNSHFCTALVLTFLFAFASNTIVLSV 127  
| : |||| : | : || : : : : |||| : | : || :  
Db 63 YIYVLAADVADLLISTVLPFSALFEVLGYMAFRVCINAAVDYLCTASTIGLCITSI 122  
| : |||| : | : || : : : : |||| : | : || :  
OY 128 DRYLSIHPLSPSKMTORRGVLLYGTVIAALDOSTPPPLYGMWGQAERDNALCSMTMG 187  
| : |||| : | : |||| : | : || : : : : |||| : | : || :  
Db 123 DRICGVSPLRKPTIVTQGRGLMALCYWALSIVLSIGPLFGMRQPA--PEDETTCOI--N 179  
| : |||| : | : |||| : | : || : : : : |||| : | : || :  
OY 168 ASPSTIIISVSFYIPIPLVIACSVYPCARQHALLNVKRSLSEVRKYDCVENDE 247  
| : |||| : | : || : : : : |||| : | : || :  
Db 180 EEPGVLFPSAGSFLPLAILIWMCRVYVAKR-----ESRGL 218  
| : |||| : | : || : : : : |||| : | : || :  
OY 248 EGAEKKEEFODESEFPRRHOEGEAKEGRMKAOGSLAKEGSTGTSSSYEARGESEVR 307  
| : |||| : | : |||| : | : || : : : : |||| : | : || :  
Db 219 KSGLKTDSDSQVTLRIHRKNRA-----GGSMASAKRTHTSFVAL- 261  
| : |||| : | : || : : : : |||| : | : || :  
OY 308 ESSTVASDGSMGKGEGSTKVEENSMKADKGRTENVOCSIDLGEDDMEEGDINFSEDDV 367  
| : |||| : | : || : : : : |||| : | : || :  
Db 262 -----LKFSPRK- 268  
| : |||| : | : || : : : : |||| : | : || :  
OY 368 EAVNPESLPSPRRSNSNPPLRCYCOKAKAVIFIIIFSYYLSLGPFCFLAVLANWVDV 427  
| : |||| : | : || : : : : |||| : | : || :  
Db 269 -----KAKTLDIIVGCVELMLPR-FVMPRGSEFP 299  
| : |||| : | : || : : : : |||| : | : || :  
OY 428 ETNQPOWVTIILIWFPLQCCHPVVYGYMKTIKEIODMKRFCEKPEKPKDS---- 483  
| : |||| : | : |||| : | : || : : : : |||| : | : || :  
Db 300 DKPSSETYFKIYWTGLINSCLNPITTYCCSOEFKAFQNWDRIOCLKRKOSSKHALGYT 359  
| : |||| : | : || : : : : |||| : | : || :  
OY 484 -HPDLPGTEGTEGKI-VPSYDSATF 507  
| : |||| : | : || : : : : |||| : | : || :  
Db 360 LHPQSAVEGGHKMDVRIIPVGSREF 385  
| : |||| : | : || : : : : |||| : | : || :

RESULT 9  
JH0315  
serotonin receptor 1A - rat  
N.Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 12-Feb-1993 #sequence Revision 12-Feb-1993 #text-change 13-Aug-1999  
C.Accession: JH0315; A35181  
R.Fujiwara, Y.; Nelson, D.L.; Kashihara, K.; Varga, E.; Roeseke, W.R.; Yamamura, H.I.  
Life Sci. 47, 127-132, 1990  
A>Title: The cloning and sequence analysis of the rat serotonin-1A receptor gene.  
A:Reference number: JH0315; MUID:90355775  
A:Accession: JH0315  
A:Molecule type: DNA  
A:Residues: 1-422 <FU>  
R.Albert, P.R.; Zhou, O.Y.; Van Tol, H.H.M.; Bunzow, J.R.; Civelli, O.  
J. Biol. Chem. 265, 5825-5832, 1990  
A>Title: Cloning, functional expression, and mRNA tissue distribution of the rat 5-hy  
A:Reference number: A35181; MUID:90202832

```

A:Accession: A35181
A:Molecule type: DNA
A:Residues: 1-372, 'S', 374-422 <ALB>
A:Cross-references: GB:J05276; NID:q202540; PIDN:AAA0612.1; PID:q202541
C:Superfamily: Vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
F:37-62/Domain: transmembrane #status predicted <TM1>
F:74-96/Domain: transmembrane #status predicted <TM2>
F:109-134/Domain: transmembrane #status predicted <TM3>
F:153-178/Domain: transmembrane #status predicted <TM4>
F:252-277/Domain: transmembrane #status predicted <TM5>
F:346-371/Domain: transmembrane #status predicted <TM6>
F:379-404/Domain: transmembrane #status predicted <TM7>

Query Match 12.5%; Score 331.5; DB 2; Length 422;
Best Local Similarity 23.5%; Pred. No. 4.5e-15;
Matches 111; Conservative 76; Mismatches 181; Indels 105; Gaps 12;

QY 26 ISLAHGIRSTVLIFFLAASFGVN--IVLALVLOKRPOLQVNTNRTFNLVTDLQISL 83
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
b 31 VTFSYQVITSLGLTIFCAVLGNACVVAIALER--SLQNVANYILGLSLAVTDLAMSVL 88
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 84 VAPWVAATSPLEPLNSHFCALVSLTHLFAFASVNTIVLVSDRYLSIHPLSYPSKM 143
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 89 VLPMAALYQVLMKWTLCQVTCDFIALDVLCCTSILHLCAALDRYWAITDPIDYVNRK 148
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 144 TORGCYLLVCTWVIALVLOSPTPLXGNGQAFDERNALCSIMGASPYTLISVFSFTI 203
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 149 TPKRAAALISLTWLTGLFSLIPPLGWRTP--EDRSDPDCTCKDHGYTYSFGAFYI 206
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 204 PLIYMIACYSVFECARROHALLYVNRHSLVLRKDCVENEDEGAKEEFODESEFR 263
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 207 PLILMLVLVGLIFFAAR-----FRIRKTVRVEKKA----- 238
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 264 ROHEGEVAKAGRMBAKDSLAKEGSTGTSSESVFARGSEVESESTVASDGMSEK 323
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 239 -----GTS-----LGTSSAPPRKSLNGCPG 259
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 324 S---TKVEENSMKADKGRTEVNOCSIDLGEDMEGEDDINFSDDEAV--NIPESLP-P 378
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 260 SGMRRCAEN-----RANGTPCT---NCAVRQGDDEATLEVIEVHRGNSKEHLPLP 308
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 379 SRRNSNSNP-----LPRCYQCAKAVIFIIIFSIVLSLGPYCFELAVLA 422
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 309 SESSNSVAPRCLEKRNERNNAEKRMALAEKRTVLTIGIMTFILCMLPEFVALVL 368
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 423 VAVVVEVQVQWVTTIILWFELQCCIHPIYVGYGMHTIKKEIDMLKKFFCK 475
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 369 PFCENSCHMPALLGAIINMGLYSNLSLNPVIYAYFNKDFQNAFKRIIKCKPCR 421
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
A35375
alpha-1-adrenergic receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A35375
R:Schwinn, D.A.; Lomasney, J.W.; Lorenz, W.; Szklut, P.J.; Fremean Jr., R.T.; Yang-Feng,
J. Biol. Chem. 265, 8183-8189, 1990
A:Title: Molecular cloning and expression of the cDNA for a novel alpha-1-adrenergic rec
A:Reference number: A35375; MUID:90243698
A:Accession: A35375
A:Molecule type: mRNA
A:Residues: 1-466 <SCGH>
A:Cross-references: GB:J05426; NID:g162663; PIDN:AAA30374.1; PID:g162664
C:Superfamily: Vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

Query Match 12.3%; Score 325.5; DB 2; Length 466;
Best Local Similarity 20.4%; Pred. No. 1.3e-14;
Matches 107; Conservative 76; Mismatches 182; Indels 157; Gaps 10;

QY 7 NSTRESNSHTCMPLSKMPSISLAHGIRSTVLIFFLAASFGVNTIVLALVLOKRPOLQVNT 66

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Db 7 NASDSSNCTH-----PPPPVNIKAILLGLGLLIFGLVGLNILEVILVSACHRHLSVT 61
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 67 NRRIFNLVTDLQISLVAPWVAATSPLEPLNSHFCALVSLTHLFAFASVNTIVLV 126
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 62 HYIIVLAADVADLLTSTVLPFSAFIEFLGVAGRVFNMAVADVLCCTASMGICITS 121
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 127 VDRYLSIHPLSYPSKMTORGVLLLYGTWIVAILLOSTPPLXGNGQAFDERNALCSMTW 186
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 122 IDRTICGSYLRKPTIYVTKRGMLLQVWALSIVLSIGLFGWRQPA--PEDETICQI-- 178
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 187 GASPSYTLISVSFFIYPLIYMIACYSVFECARROHALLYVNRHSLVLRKDCVENE 246
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 179 NEEPGYLFSALGSFYPLTIIILMYCRVYVAVK----- 213
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 247 EFGAKKEEFODESEFRROHEGEVAKAGEGMEAKKDSLAKEGSTGTSSESVFARGSEEV 306
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 214 -----ESRG----- 217
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 307 RESSTVASDGMSEKGEKSTKVEENSMKADKGRTEVNOCSIDLGEDMEGEDDINFSED 366
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 218 -----LKSLKTKDSDS---EQYTLRIHRKNNOVGSGVTSKNNTHFSVRLKFSREK 268
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 367 VEAVNIPESLPSSRRNSNPPLPRCYQCAKAVIFIIIFSIVLSLGPYCFELAVLAWVD 426
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 269 -----KAAKTLGIYVCFVLCMLPF--FLVMPIGSEF 298
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 427 VENVQVQWVTTIILWFELQCCIHPIYVGYGMHTIKKEIDMLKKFFCKRPPK----- 480
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 299 PDFPSETVKRIAFWGLYVLCINPIIYPCSSQEFKAFQNVNLRIOCKRKQSSKHTLGT 358
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 481 -----EDSHPDL-----PGTEGTEGRIVPS 501
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 359 TLAHPSHVLEGOKHDLVIRIPGSAEFPYKISKTDGVCEMKIFPS 402
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
A47174
serotonin receptor - great pond snail
N:Alternate names: 5-hydroxytryptamine receptor (5-HTR)
C:Species: Lymnaea stagnalis (great pond snail)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: A47174
R:Sugamori, K.S.; Sunahara, R.K.; Guan, H.C.; Bulloch, A.G.; Tensen, C.P.; Seeman, P.
Proc. Natl. Acad. Sci. U.S.A. 90, 11-15, 1993
A:Title: Serotonin receptor cDNA cloned from Lymnaea stagnalis.
A:Reference number: A47174; MUID:93126323
A:Accession: A47174
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-509 <SUG>
A:Cross-references: GB:U06803; NID:g159458; PIDN:AAA29290.1; PID:g159459
A:Experimental source: central nervous system (NCBIN:121945, NCBI:P:121952)
C:Superfamily: octopamine receptor type I
C:Keywords: neurotransmitter receptor

Query Match 12.1%; Score 319; DB 2; Length 509;
Best Local Similarity 22.3%; Pred. No. 3.9e-14;
Matches 108; Conservative 96; Mismatches 205; Indels 76; Gaps 14;

QY 3 STCTNSSTRESNSHTCMPLSKMPSISLAHGIRSTVLIFFLAASFGVN--IVLALVLOKRP 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 74 TSATNMETDDRWMSLTIV-----YSHHVLVTSVILGLFVLCIIGCFVIAVMLEER-- 124
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 QLVQVNRRTFNLVTDLQISLVAPWVAATSPLEPLNSHFCALVSLTHLFAFASVN 120
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 125 SLHVAANYILISLAVADLMAVAVLWVPLSVSELSKWFLESEVCDMWISVDVLCCTASIL 184
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 121 TIVLVSDRYLSIHPLSYPSKMTORGVLLLYGTWIVAILLOSTPPLXGNGQAFD--ERN 179
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 185 HLVAAMDRIWAAT--SIDYLRKRSARRILMLIMVYVIALVLPISLPPLFGMRDPNPDCKT 243
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_FL\_1; 1.  
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
SQ SEQUENCE 455 AA; 50802 MW; 80C60918FA6086C CRC64;

Query Match 12.8%; Score 338.5; DB 4; Length 455;  
Best local similarity 21.3%; Pred. No. 8.9e-18;  
Matches 108; Conservative 80; Mismatches 187; Indels 131; Gaps 11;

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QY 8 STESNSHICMPLSKMPLSLANGIIRSYLVIFLAAPFNGNIVLAVLQKROLQVYN 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5 SGNADSSNCTQP--PAPVNIKAILGLVLLGGLIFGVGNILVLSVACHRLHSVTH 62
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 68 RTFNLVTDLOISLVAAPVAVTSVPLFPLNSHFCETALVSLTHLFAFASVNTIVLVS 127
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 63 YVIVNLAVADLLSTVLPSPSAIFEVIGYNAFGVPCNIMAADVLCCTASIMGLCTIST 122
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 128 DRYLSITHLPSPSKMTQRRGYLLVLTGTVIALIQTTPPLYGMOQAADERNALCSMIMG 187
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 123 DRYIGVSPLEPYPIYQRRGLMALLCVMALSLIVISIGPLFGWQPA-PEDETICQT--N 179
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Y 188 ASPSYTILSVSFIVIPLIYMIACYSVFCARQHALLVNKRHSLEVRKOCVENEDE 247
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 180 EEPGEYVLEFSLGSPFLPLAILVWYCRVYVAKR-----ESRGL 218
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 248 EGAEEKFEFQDESEFRQHEGEVAKEGRMKADGSLAKEGSTGTSESSVEARGSEEV 307
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 219 KSGIKTKKSSEQVTLIRHKNA-----GGSGMASATKTHFSVRL- 261
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 308 ESSTVASDGSMEKEGSTKVENSMKADGRTEVNOCSIDLGEDDMFEGDDINFSDDV 367
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 262 -----LKFSREK- 268
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 368 EAVNIPEPSLPSPRNSNSNPRLRCYCCKAAKVIITIIISYVLSLPGYCFALAVWVDV 427
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 269 -----KAAKTGLIVGCFELCWPPLF-FLVMIGISFP 299
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 428 EFOVQPWVITIIIMFLFLOCCIHPPYVGYMHKTIKKEIODMLK-KFCKEKPPE---D 482
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 300 DFKPSEVFEFVIVLWGLTNCINPIITPCSSQEPKAFQVNLRIQCLCRKSSKHALGYT 359
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 483 SHDLPETEGTEGKI-VPSYDSATF 507
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 360 LHPPQAVEGQHKDMVRIPVGSRETF 385
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 11
AC 09N296 PRELIMINARY; PRT; 422 AA.
ID 09N296
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SEROTONIN RECEPTOR 1A.
GN HTR1A.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.
OX NCBI_TaxId=9600;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORAN-POL3;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
CC Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL; AB041406; BAA94491.1; -.
DR HSSP; P29274; 1MMH.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
```

DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_FL\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
SQ SEQUENCE 422 AA; 46121 MW; C2CC9803BEF89B CRC64;

Query Match 12.7%; Score 335.5; DB 6; Length 422;  
Best local similarity 22.5%; Pred. No. 1.4e-17;  
Matches 104; Conservative 89; Mismatches 187; Indels 83; Gaps 10;

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QY 26 ISLAHGIRSTVLAIFLAASFVGN--IVLAVLQKROLQVYNRFNFNLVTDLOISL 83
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 31 VTFEYOVTLSLGLTLFPCVNLGACVAAIALER--SLQVANNVILGSLAVTDLWVSVL 88
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 84 VAPVAVTSVPLFPLNSHFCETALVSLTHLFAFASVNTIVLVSVDRLSLIHPSPSKM 143
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 89 VLPMALVQVLNKKWTIGQVQCDFIALDVLCCTSSILHLCAIALDRWMTATDIDVYK 148
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 144 TORRGVLLYGTWIVIALIQTTPPLYGMOQAADERNALCSMIMGASPTIISVSFIV 203
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 149 TPRRAALISLFWLIGFLISIPPLGWRP--EDRSDPDACITSKDHGYTISFGAFYI 206
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 204 PLIVMIACYSVFCARQHALLVNKRHSLEVRKOCVENEDEBGA-----EKK 253
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 207 PLMLVLVGRITRAAR-----PRIKRTYKAVERTGADTHHGASPAPOK 251
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 254 EEPQDESEFRQHEGEVAKEGRMKADGSLAKEGSTGTSESSVEARGSEEVRSSTVA 313
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 252 KSVNGESGSNNWRIG-VESKAGGGLCANAV--RQGDGAALVEIVH----- 296
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 314 SDGSMEKEGSTKVENSMKADGRTEVNOCSIDLGEDDMFEGDDINFSDDVEAVNIP 373
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 297 -----RVGNSK-EHLPLPSEAGPTPCAPASPE----- 322
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 374 ESLPSPRNSNSNPRLRCYCCKAAKVIITIIISYVLSLPGYCFALAVWVDVQVPQ 433
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 323 ---RKNERNAEAKKMLADERTVKTGLIMGFILCWPFLVAVLDPFCSSCHMPT 379
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 434 WVITIIIMFLFLOCCIHPPYVGYMHKTIKKEIODMLKPFCKE 476
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 380 LLAGIIMWLGTSNLNPVYIAVFNKDFQNAFKKIICKRCRQ 422
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

```
RESULT 12
ID 013729 PRELIMINARY; PRT; 429 AA.
AC 013729;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ALPHA 1C ADRENERGIC RECEPTOR ISOFORM 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Tanaka T.;
RT Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 424-429 FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=9525557; Pubmed=7737411;
RA Murasawa A., Shibata K., Horie K., Takei Y., Obika K., Tanaka T.,
RA Muramoto N., Takagaki K., Yano J., Tsujimoto G.;
RT Cloning, functional expression and tissue distribution of human alpha
RT 1c-adrenoceptor splice variants.";
RL FEBS Lett. 363:256-260(1995).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; D32201; BAA06900.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
```

RL	Moj. Brin Res.	47:67-77(1977).
CC	-1-	SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1-	SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL:	Y07901; CAAB69208.1; -.
DR	HSSP;	P29274; IMM.
DR	InterPro;	IPIR000276; GPCR_Rhodopsn.
DR	Pfam;	PF00001; 7tm.1; 1.
DR	PRINTS;	PR00237; GPCRRHODOPSN.
DR	PROSITE;	PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR	PROSITE;	PS50262; G-PROTEIN_RECEP_FL2; 1.
KW	G-protein coupled receptor;	Glycoprotein; Receptor; Transmembrane.
SEQUENCE	408 AA;	45787 MW; 2CB6156F7D53B1b5 CRC64;
SO		
Query Match	12.8%;	Score 339.5; DB 13; Length 408;
Best Local Similarity	24.8%;	Pred. No. 6.5e-18;
Matches	114;	Conservative 78; Mismatches 187; Indels 81; Gaps 14;
OY	23	KMPISLHGIIIRSYTLVLEAFVGN--IYVALDKRPOLQOYTNRIFNLATDLIQ 80
Dd	24	RCPVS-IQLIASLFLGFSFGITGMNCVIAIALER-SLOANYANLYIGSLAVTDLVW 79
OY	81	ISLVAIPVVATSVLPFWPLNSHFCTALSLTHLFAPASNYTIVLSVDRYLSIHPLSP 140
Dd	80	SVLVLPMAQNQVLKMKWTLLGOYTCDIFISLDVLCSTSLHLCAIALDYAINTPIDIV 139
OY	141	SKMTDRRGILLGYTVIAIILDSPTPLPYGWGAADFERNALCSMTMGASPSTIIISVVF 200
Dd	140	NKRFPFRRAVLTISIWIIVGISISIPPMGLWRPP-EDRSNPACRISEDPGYTIYSTFGA 197
OY	201	IYIPLIWIACSVYFCARQHALLYNKRISLEVYAKDCVENDEBEAAKEEKPQDS 260
Dd	198	FYIPLILWLVLGKIETFKRAR-----FRIKTYKK-----AEKK----- 230
OY	261	EFRROHEGEVNAKEGRMAKDGLSAKEEGSTGTSSESYEARSGEEVRESSTVASDGSMCG 320
Dd	231	-----KYADICLSVQSQSPREKQ--REAQGLEEVGGAQNR-----CVNGAIRBG 274
OY	321	KEGSTVEBNMSKAKDKRTENV-QCSDIDGEDDMERGDDINFSEDDEAVAINIPESLPS 379
Dd	275	EGAV-----LEIEVHHVYNSKCHL-----HCKFVPPEPOLPPA 309
OY	380	RNN---SNSNPRLPRCYOCKAKAYFIIFIISVYLSLGPCELAVALAWWDVETQPQWVI 436
Dd	310	LKNDRATEKKRKVALAREKVTKTGITIGMFTYLCLWPFLYVALVPCEY-CHMHPLL 368
OY	437	TIIMLFELQCIHPYVYGMYHKTKKETQDIOMLKRFCKE 476
Dd	369	DIITMLGYSNLSLNPIIYAFENKDKQSAFKIIRKCFKQ 408
RESULT 9		
ID	O9N297	PRELIMINARY: PRT: 422 AA.
NC	O9N297,	
DT	01-OCT-2000 (TREMBLrel. 15,	Created)
DT	01-OCT-2000 (TREMBLrel. 15,	Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19,	Last annotation update)
DE	SEROTONIN RECEPTOR 1A.	
GN	HTFA.	
OS	Gorilla gorilla (gorilla).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.	
OX	NCBI_TaxID=9593;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-GORILLA-UI;	
RA	Kitano T., Kobayakawa H., Saitou N.;	
RT	"Silver Project."	
RL	Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.	
CC	-1-	SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR	EMBL:	AB041405; BAA94490.1; -.
DR	HSSP;	P29274; IMM.

DR	InterPro: IPR000276; GPCR_Rhodopsn.
DR	Pfam: PF00001: 7tm.1: 1.
DR	PRINTS: PR00237; GPCRHHODOPSN
DR	PROSITE: PS00237; G-PROTEIN_RECP_F1.1; 1.
DR	PROSITE: PS50262; G-PROTEIN_RECP_F1.2; 1.
KW	G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SD	SEQUENCE 422 AA; 46154 MW; 012335E0403F1B90 CRC64;
	Query Match 12.8%; Score 339.5; DB 6; Length 422;
	Best Local Similarity 22.0%; Pred. No. 6.8e-18;
	Matches 101; Conservative 91; Mismatches 191; Indels 77; Gaps
OY	26 ISLNGIIRSYVLVFLFVLAAPVGN--IYLAIVLQKKPOLQVYTNRFPLVTLDTLLQSL 83
DB	31 VTESVQVTSLSLGLTGLIFCAVAGNCAVVAIALER--SLQNAANTLIGSLAVTDLWVSL 88
OY	84 VAPVAVATSVLPFWPLNHSFCTALSLTHLFAFASVNTVLVSVDVRLSIHPLSPSKM 143
DB	89 VLPMAALVQLNKKMLGQVLTQDLFLADVLCTSSLIHLCAIALDRYMAITPDIYVKR 148
OY	144 TORRGYLLLYGTVAIVALLQSTPPRLPYGCGAFAFERNALCMTMGASPTTILSVSEIYI 203
DB	149 TPRRAAALISLTWLIGFLTISIPMLGWRP--EDRSSDPACTISKDGHGTYITSTGAFYI 206
OY	204 PLIVVIACYSVYECARRHALLVWKRISLEVRKDCYENDEDEGAKEKEEFODESER 263
DB	207 PLLMLLVLYGRIFEAR-----FRIRKTYKKVEKKGADLRHGASPAPOK 251
OY	264 ROHEGEVAKKEGRM--EAKDGSL-----KAKGSGTSGSESVARGSEEVRESSTVASDG 316
DB	252 KSVNGESGSRMRRLGVESAGALCANGAVRGGDGALEIVH----- 296
OY	317 SMEGEGSTKYEVNSMKADKGRTEVYNQCSIDIGEDDMFEGEDINSEDDVEAVNIPESL 376
DB	297 ----RVGNK-EDHLPDSAGPTPCAPAPAF----- 322
OY	377 PSKRNSNSNPPLPRPCYQCKAKAVFIITFFSVLSGPRCFIAYLVAVWDEVQYPOWYI 436
DB	323 RKNENAEKKRMALAREKRYTKTIGITIGTFLCMLPFIYALVLPFCSSCHMPTLLG 382
OY	437 TTIIMLFLOCCIHPPVYGYMKHTIKKEIQQDIKKFFCKE 476
DB	383 AIIIMLGYNSLNPYIYAVFPKKDQNAKKRIIKCFKQ 422
RESULT 10	
ID	060451 PRELIMINARY; PRT: 455 AA.
AC	060451.
DT	01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	ALPHA 1A ADRENERGIC RECEPTOR ISOFORM 4.
OS	Homo sapiens (Human)
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=PROSTATE;
RX	MEDLINE=98149668; PubMed=9490024;
RA	Chang D.J., Chang T.K., Yamanishi S.S., Salazar F.H.R., Kosaka A.H.,
RA	Khare R., Bhakta S., Jasper J.R., Shieh I.-S., Lesnick J.D.,
RA	Ford A.P.W., Daniels D.V., Clarke D.E., Bach C.T., Chan H.W.,
RT	"Molecular cloning, genomic characterization and expression of novel
RT	human alpha1-adrenoceptor isoforms."
RL	FEBS Lett. 422:279-283(1998).
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL: AF013261; AAC06138.1; -
DR	InterPro: IPR000276; GPCR_Rhodopsn.
DR	Pfam: PF00001; 7tm.1; 1.
DR	PRINTS: PR00237; GPCRHHODOPSN

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxId=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RQ STRAIN-BRED NEW ZEALAND WHITE;  
RX MEDLINE=20243335; PubMed=10780960;  
RA Suzuki F., Taniguchi T., Takaiji R., Murata S., Muramatsu I.,  
BT J. Pharmacol. 129:1569-1576 (2000).  
RL "Splice isoforms of alpha(1a)-adrenoceptor in rabbit.";  
CC -1- SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN (BY SIMILARITY)  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL: AF157506; AAF80169.1; -.  
DR HSP: P02699; 1F88.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHHODPSN.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
SQ SEQUENCE 425 AA: 47009 MW; 1202C83BF7644CB CRC64;

Query Match	12.9%	Score 340;	DB 6;	Length 425;
Best Local Similarity	22.0%	Pred. No. 6.3e-18;		
Matches 102;	Conservative 73;	Mismatches 161;	Indels 128;	Gaps 9;

9.

Oy	7	NSTRSSNSHRCMPLSKMPTSLAHGIRSVYFLFLAASVGNVIALVQRRPOLLOYT	66
Dd	7	NASSOSSNCHT-----PAPVAVISAKAILLGVILGGLIFGVGNILVILSACHRHLSHYT	61
Oy	67	NRETFNLVYDLDLOISLVAPVAVATSVLPFLMPLNSHETALVSLTHLFAFASVNTIVLVS	126
Dd	62	HYIYVNLVADLDLTLSTVLPFSALFEIILGVAFGFVRCNCIMAAVDLCCASTISLSEVLS	121
Oy	127	VDRYLSIIHPLSVESKMTORRGVILLYLGTWVIALLOSTPRPLXMGQAAFDERNAALCSMT	186
Dd	122	IDRIGVSYPLRYPLFYVQRRGLRALLCVAWFSVLIVSIVGFLFGRODAPPD-ETTCOI--	178
Oy	187	GASPSYTLVSVSEFIVPLVIMACYSVFCAARQHALLNYNRHSLSEVRVAKDCVENED	246
Dd	179	NBPFGVYLFSALGSPFYVPLTILMLCYRVVYVAKR-----ESRG	217
Oy	247	EEGAAKKEEFODESEFFRRQHEGVAKACEGRMEAKDGLAKKEGSTGTSSESSVEARGSEEV	306
Dd	218	LKSGLKTDKSDSEGVYTLRIHRKNRPA-----GSGVYASA-----	251
Oy	307	RESSVVASDGSMEKKEGSTVKEENSKMAKDRGTEVQNCSTIDLGDDMEFGEDDINFESDD	366
Dd	252	-----KNKT-----HESVRLKTSRREK	268
Y	367	VEAVNIPESLPSRRNSNSNPRLRCYQCKAAKVIIFIIFESYVLSLGRYCFLLAWMD	426
Dd	269	-----KAAKTLGIWCGFVLCMLPFL-FLVMPIGSGF	298
Oy	427	VEYQVQPMVYIITIIWFFLQCSHPRUYGYGHNKTIKKEIDMYL	470
Dd	299	PDEKRPETVEKIVEMWGLGNSCINPDIITPCSSQGEFFKAFONVVK	342

RESULT 7	
Q9MZU3	
ID	Q9MZU3
AC	Q9MZU3;
DT	01-OCT-2000 (Tremblrel, 15, Created)
DT	01-OCT-2000 (Tremblrel, 15, Last sequence update)
DT	01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE	ALPHA 1A-ADRENOCEPTOR ISOFORM 2.
OC	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_TaxID=9986;
RN	[1]
RP	SEQUENCE FROM N.A.
RF	STRAIN-BREED NEW ZEALAND WHITE;

RX MEDLINE=20243335; PubMed=10780960;  
RA Suzuki F., Taniguchi T., Takaya R., Murata S., Muramatsu I.,  
RT "Splice isoforms of alpha(1a)-adrenoceptor in rabbit.";  
RL Br. J. Pharmacol. 129:1569-1576 (2000).  
RC -1. SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN (BY SIMILARITY)  
CC -1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EML: AFI57505; AAF80168.1; -  
DR HSP: P02699; 1F88.  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHOOPSn.  
DR PROSITE: PS00237; G\_PROTEIN\_REEP\_FL\_1; 1.  
DR PROSITE: PSS0263; G\_PROTEIN\_REEP\_FL\_2; 1.  
KW G-protein coupled receptor, Glycoprotein, Transmembrane.  
SQ SEQUENCE 429 AA; 47463 MW; F907B487FEE6D83B CMC64;

Query Match	12.9%;	Score 340;	DB 6;	Length 429;
Best Local Similarity	22.0%;	Pred. No. 6.3e-18;		
Matches 102;	Conservative 73;	Mismatches 161;	Indels 128;	Gaps 9

9

[illegible]

ID	PRELIMINARY:	PRT:	408 AA.
098998			
AC	Q98998		
DT	01-FEB-1997 (TREMBLrel. 02, Created)		
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	5-HT1A RECEPTOR.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RX	MEDLINE=97364954; PubMed=9221903;		
RA	Marracci S., Chui D., Nardi I.;		
RT	"Cloning and developmental expression of 5-HT1A receptor gene in		
RT	Xenopus laevis.";		

[illegible]

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DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SEROTONIN RECEPTOR 1A.
GN HTR1A.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
CX NCBI_TaxID=9558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHMP-220;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SOURCE/CELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB041404; BAA94489.1; -.
DR HSSP; P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR K W G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 422 AA; 46171 MW; FCD989BD013A1A0 CRC64;

Query Match 12.9%; Score 340.5; DB 6; Length 422;
Best Local Similarity 22.0%; Pred. No. 5,7e-18;
Matches 101; Conservative 91; Mismatches 191; Indels 77; Gaps 9;

OY 26 ISLAGIIRSYLVVIFFLAASPVGN--IVALVLRKPOLQTYNRTFNMLTYDLDLSL 83
DB 31 VFEYSQVYVITSLGLTFLICFAVLGNCVVAIALER--SLQANANVLIGSLAVTDLWVSL 88
OY 84 VAPWVAVTSVPLFEPPLNSHFTALVSLTFLFAFASVNTIVLSVDRLSIHPLSPSKM 143
DB 89 VLPMAALVOYLKNTILGQYTCDFIALDVLCCTSSILHLCAIALDRYMAITDPIDYVKR 148
OY 144 TQREGVLLTGYTIVAILLOSTPEPLXWGGAEDERNALCSMTIGASPSYTLISVSFVI 203
DB 149 TPRRAAALISLWTLIGFLISIPPMIGWRRP--EDRSDDPACTISKDHGYTISTFGAFYI 206
OY 204 PLIVMIACSVYFCARRHALLINVKRSLSEYKVDQYENDEDEBAEKKKEFQDSSEFR 263
DB 207 PLLIMLVILGRIFRRAR-----FRIRKTYKKVEKGACADRRHGASPAQOPK 251
OY 264 ROHEGVEYKKEGRM--EAKDGSL-----KAKGGSTGSSSEYARGSEVRRESSVASDG 316
DB 252 KSYVNGESGRNKRNLGVESASGALCANGAVROGDCAALEVIEVH----- 296
OY 317 SMEKGEGSKYVEVENSKKADKGRTEVNOCSIDLGEDDMEGEDDINFSDDVEAVNIPESL 376
DB 297 ----RGNKSK-DHPLPSPSAGPTPCAPASFE----- 322
OY 377 PPSRNSNSNPPLPRCYQCKAAKVFITITFSVLSIGPYCFLAVLAWVDVETQVQWYI 436
DB 323 RKNENNAEKRRMALARERKVTKTIIGITIGFTILCLPFIYALVLPFCSSSCHMPTLLG 382
OY 437 TTIIMLFLOCCIHPPVYGYMKTKIKELIODLKKRFCKE 476
DB 383 AIIIMLVGYSNLSLNPVIAVFMKDFONAEKFKIKCFKQ 422

RESULT 6
O9MZU2
ID O9MZU2 PRELIMINARY; PRT: 425 AA.
AC O9MZU2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ALPHA 1A-ADRENOCEPTOR ISOFORM 3.
OC Erythrocytus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Db	121	TIIVVSDRYLIIHPLISYPSKMKQRGRGVLIXGTWITVALIGSPPLVGMGOAFBERNA	180
Qy	181	LCSMWGASPSYITLLVVSFTVLPDIYMIACISVYFCABRQHALLYNKRHSLEVAVKD	240
Db	181	LCSMWGASPSYITLLVVSFTVLPDIYMIACISVYFCABRQHALLYNKRHSLEVAVKD	240
Qy	241	CVEENDEGAKKKEEPDDESEFRQHGVEKAKGRRAREKDGSLKAKEGSTGTSSEVFA	300
Db	241	CVEENDEGAKKKEEPDDESEFRQHGVEKAKGRRAREKDGSLKAKEGSTGTSSEVFA	300
Qy	301	RGESEVERESTVVAADSGMECKEGSTKYEENSMKADKCRTEVNOCSIDLGEDDMFEGDDI	360
Db	301	RGESEVERESTVVAADSGMECKEGSTKYEENSMKADKCRTEVNOCSIDLGEDDMFEGDDI	360
Qy	361	NFSEDDYEAVNIPESLPPSRNRNSNPNPRLPCRYOCKAAYIFIIITSYVSLGPRCYFLAV	420
Db	361	NFSEDDYEAVNIPESLPPSRNRNSNPNPRLPCRYOCKAAYIFIIITSYVSLGPRCYFLAV	420
Qy	421	LAVWVDYETQVPQWVITIIIMFLQCCIHPIYVYGYNHKKITKKEIDMLKKFPCKEKPRK	480
Db	421	LAVWVDYETQVPQWVITIIIMFLQCCIHPIYVYGYNHKKITKKEIDMLKKFPCKEKPRK	480
Qy	481	EDSHDPLPGTEGGTEGKIIVPSYDSATPR	508
Db	481	EDSHDPLPGTEGGTEGKIIVPSYDSATPR	508

ID	Q90X46	PRELIMINARY:	PROT:	402 AA.
AC	Q90X46:			
DT	01-DEC-2001	(TREMBLrel, 19, Created)		
DT	01-DEC-2001	(TREMBLrel, 19, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel, 19, Last annotation update)		
DE	SC:BZ2015.4	(NOVEL PROTEIN SIMILAR TO HUMAN G-PROTEIN COUPLED RECEPTOR RE2):		
DE	SC:BZ2015.4.			
GN	Brachydanio rerio (zebrafish) (Zebra danio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;			
OC	Cypriniformes; Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RL	Lloyd D.;			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL590146; CAC94897.1; -.			
RW	Receptor.			
SO	SEQUENCE	402 AA; 44373 MW; 5FB8875874267F00 CRC64;		
Query Match		14.8%; Score 392.5; DB 13; Length 402;		
Best Local Similarity		23.8%; Pred. NO. 5.9e-22;		
Matches 105; Conservative		72; Mismatches 127; Indels 138; Gaps		
QY	32	IRSTVLVIFLASEFVGNIVLALVLRKRPOLQVNTREFNLVLVDLQISLAPVWVAT	91	
DB	24	VLESVSIITIIAIIACGLNIVLVLYTKRPYLTPSNKFVFSLTSSNLLSLVLMFPVVAS	83	
QY	92	SVLPFLPILNSHRC--TALVSLTHLEAFASVNTIVLSVDRIYSLIHPISYSPKMTQRCGY	149	
DB	84	SVRRDMMGVVMNCNTALLHL--LVSSSSMLTGAIAIDRYAVYAPMIVPKRTIGNRVAV	141	
QY	150	LLVLTGVTVAILQSPPLTGYMGQAAFDERNALCSIMWGASPSYTLISVVSFIVPIIVAI	209	
DB	142	LAIYIIVTHSLVGLCPPLFGMSSEFFDRFKWTCTYSWKHEISYTLAFWYTWCCLLPLVAML	201	
QY	210	ACYSVVFCARQOHALLVNKRHSLEVVRKDCVENEDDEGAERKEEFODESEFRROHEE	269	
DB	202	VCGYVIFRVAR-----	212	
QY	270	VKAKGRGHEAKDGLSKAKEDSGTGESESVANGSEFVRRESSTVVASDGSMEKESGTVEE	329	
DB	213	-----TKRVYVCG-----SYVVS-----OE	228	

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OY      330 NSMKADKGRTEVNOCSIDLGDDEDMFEQEDDINFESEDDVEAVNIPESLPERRRN---SNSN 386
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      229 ESSSSONNRKNRKSNTSTSSSG-----SRKSLIVSGS- 258
OY      387 PRLPRCYOCRAKAVIFIIIFSVLSLGPCELAVALAWVDENVQPOMWITIIIMFLQ 446
        ||| | | : : : : : ||| : : : | | | : : : ||| |
Db      259 -----QCKAFITILVLVLGFTLLTWGPPVVVISTEALLGNKNSVPQ-VETLVSWLSFTS 310
OY      447 CCIHPYVGVGMHKTIKKEIODM 468
        || :|| :|| :|| :|| |
Db      311 AVCHPLILGLMWKTKVRKELLGM 332
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[illegible]

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:42:43 : Search time 31 Seconds  
(without alignments)  
2834.885 Million cell updates/sec

Title: US-09-992-238-2

Perfect score: 2644  
Sequence: 1 MTSCTNSTRESNSHTCMP.....GTGGTEGKIVPSYDSATFP 508

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP\_TREMBL\_19:\*  
2: SP\_archaea:\*  
3: SP\_bacteria:\*  
4: SP\_fungi:\*  
5: SP\_human:\*  
6: SP\_invertebrate:\*  
7: SP\_mmc:\*  
8: SP\_organelle:\*  
9: SP\_phage:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP Vertebrate:\*  
14: SP Unclassified:\*  
15: SP\_RVirus:\*  
16: SP\_Bacteriap:\*  
17: SP\_Archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2641	99.9	508	4	Q96P66 homo sapien
2	392.5	14.8	402	13	Q90X46 brachydanio
3	391	14.8	407	4	Q75963 homo sapien
4	343	13.0	466	4	Q96R68 homo sapien
5	340.5	12.9	422	6	Q9N298 pan troglod
6	340	12.9	425	6	Q9N203 oryctolagus
7	340	12.9	429	6	Q9N202 oryctolagus
8	339.5	12.8	408	13	Q98998 xenopus lae
9	339.5	12.8	422	6	Q9N297 gorilla gor
10	338.5	12.7	455	4	Q60451 homo sapien
11	335.5	12.6	422	6	Q9N296 pongo pygma
12	333.5	12.6	429	4	Q13729 homo sapien
13	333.5	12.6	499	4	Q13675 homo sapien
14	325.5	12.3	466	11	Q54913 mus musculu
15	325.5	12.3	466	4	Q9UD63 G9ud63 homo sapien
16	324	12.3	466	6	Q9T5W7 G9T5W7 sus scrofa

17	317	12.0	571	6	Q9T5W9	Q9T5W9 sus scrofa
18	304.5	11.5	601	5	Q95YF4	Q95YF4 drosophila
19	300.5	11.4	559	11	Q9QW71	Q9QW71 rattus sp.
20	299	11.3	631	5	Q9VEG1	Q9VEG1 drosophila
21	297.5	11.3	349	4	Q9UD67	Q9UD67 homo sapien
22	291.5	11.0	461	13	Q9OM07	Q9OM07 oncorhynch
23	291	11.0	474	4	Q96R68	Q96R68 homo sapien
24	287	10.9	456	4	Q96R68	Q96R68 homo sapien
25	285	10.8	610	5	Q44986	Q44986 caenorhabdi
26	283	10.7	515	11	Q9DBL0	Q9DBL0 mus musculu
27	282.5	10.7	432	13	Q9QWY6	Q9QWY6 brachydanio
28	280	10.6	391	5	Q96716	Q96716 brachydanio
29	280	10.6	510	13	Q9QWY5	Q9QWY5 brachydanio
30	279.5	10.6	419	5	Q77254	Q77254 boophilus m
31	279	10.6	518	6	Q9MYT8	Q9MYT8 oryctolagus
32	276	10.4	440	6	Q9N2A5	Q9N2A5 pongo pygma
33	276	10.4	445	4	Q9N2R3	Q9N2R3 homo sapien
34	275.5	10.4	526	4	Q96RG7	Q96RG7 homo sapien
35	275	10.4	528	13	Q9PTF6	Q9PTF6 gallus gall
36	274	10.4	370	4	Q9H1N4	Q9H1N4 homo sapien
37	274	10.4	440	4	Q9P1X9	Q9P1X9 homo sapien
38	274	10.4	440	6	Q9N2A7	Q9N2A7 pan troglod
39	274	10.4	440	6	Q9N2A6	Q9N2A6 gorilla gor
40	274	10.4	443	4	Q9UPA9	Q9UPA9 homo sapien
41	272	10.3	477	5	Q9BMA9	Q9BMA9 mamestra br
42	270	10.2	470	11	P97842	P97842 rattus norv
43	267.5	10.1	396	4	Q9NOS5	Q9NOS5 homo sapien
44	266	10.1	392	13	Q9YHA5	Q9YHA5 myxine glut
45	265.5	10.0	414	6	Q9GK99	Q9GK99 canis famli

## ALIGNMENTS

RESULT 1  
ID Q96P66 PRELIMINARY; PRT; 508 AA.

AC Q96P66; 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE G PROTEIN-COUPLED RECEPTOR.  
GN GPR101.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21458557; PubMed=11574155;  
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arkhiko O.,  
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;  
RT "Discovery and mapping of ten novel G protein-coupled receptor  
genes".  
RL Gene 275:83-91(2001).  
DR EMBL; AF411115; AAL26486.1; -  
KW RECEPTOR.  
SQ SEQUENCE 508 AA; 56716 MW; E20A409P65C95B85 CRC64;

Query Match 99.9%; Score 2641; DB 4; Length 508;  
Best Local Similarity 99.8%; Pred. No. 4.9e-193;  
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTSCTNSTRESNSHTCMPISLAHGIRSTVLVIFLAISFGNVLALVLRKP 60  
DB 1 MTSCTNSTRESNSHTCMPISLAHGIRSTVLVIFLAISFGNVLALVLRKP 60  
QY QLVQVTRNFNLVTDLQSLVAPWVATSVLPFLNHFCTALVSLTHLFAFASVN 120  
DB QLVQVTRNFNLVTDLQSLVAPWVATSVLPFLNHFCTALVSLTHLFAFASVN 120  
QY TLIVASVDVRLSIHPLSPSKMTQVRGTYLLYGTVIALQSPPLVYGWQAAFDENNA 180  
DB TLIVASVDVRLSIHPLSPSKMTQVRGTYLLYGTVIALQSPPLVYGWQAAFDENNA 180





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QY 180 ALCNMGASPSYTLISVSVFTIPLIYMIACYSVFCAARROHALLVVKRHSLEVRYK 239
DB 244 GTC--LISODKGYTIFSTVGAFYFLPMLVMITILYIRLWLVARS-----IRDKQOMKRA 295
QY 240 DCVENDEDEGAKKEFEODESEFRQHEGYAKAGRMEA-----KDSLIK 285
DB 236 RLKTEETLIVASPKTEYSVSDSCNCSNDPTTEKKRRAPKSYGCSRPERRKKNRAKK 355
QY 286 AKEGSTGTSSESVSEARGESEVR-ESSYVASDGSMEKGSTVEENSKAKDGREVNOC 344
DB 356 LPERANGVNSNSSSERLKQIETIAEAFANCAE--EASTAMLE-----RQC 401
QY 345 SIDGEDMEFGEEDDINFSEDDVEAVNIPESLPPSRNNSNPNPLRCYOCKAAKVFIFI 404
DB 402 N-----NGKRTISSNDTPYSRTREKLEKRR-----KAARTLAI 436
QY 405 IFSVYLSGPGYCLAVLAWVDVETQVQWITITIIWFLQCCIHPIVYGMHTIKKE 464
DB 437 TGAFLICWLPFFITALLISPFVDPE-GIPFARSFVLMWGYNSLNPITITIFSPERSA 495
QY 465 IQDML 469
DB 496 FOKIL 500

RESULT 15
ALAD_MOUSE STANDARD: PRT: 562 AA.
ID ALAD_MOUSE
AC P97714; 061619;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
DE adrenergic receptor).
GN ADRALD OR ADRALA OR GPCR8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=56064818; PubMed=7595531;
RA Alonso-Llamazares A., Zamanillo D., Casanova E., Ovalle S., Calvo P.,
RA Chuchetru M.A.;
RT "Molecular cloning of alpha 1d-adrenergic receptor and tissue
RT distribution of three alpha 1-adrenergic receptor subtypes in
RT mouse.";
RL J. Neurochem. 65:2387-2392(1995).
RN [2]
RP SEQUENCE OF 190-350 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=54116980; PubMed=8288218;
RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
RA Copeland N.G., Jenkins N.A.;
RT "Identification, chromosomal location, and genome organization of
RT mammalian G-protein-coupled receptors.";
RL Genomics 18:175-184(1993).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
CC THROUGH THE INFUX OF EXTRACELLULAR CALCIUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; S80044; ABA47042.1; -

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DR EMBL; L20333; AAA16854.1; -
DR GCRdb; GCR_0810; -
DR GCRdb; GCR_1976; -
DR MGD; MGI:106673; Adrald.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; transmembrane; glycoprotein;
KW Multigene family; phosphorylation; lipoprotein; palmitate.
KW Domain
FT DOMAIN 1 90
FT TRANSSEM 91 115
FT DOMAIN 116 127
FT TRANSSEM 128 153
FT DOMAIN 154 163
FT TRANSSEM 164 186
FT DOMAIN 187 207
FT TRANSSEM 208 232
FT DOMAIN 233 245
FT TRANSSEM 246 269
FT DOMAIN 270 342
FT TRANSSEM 343 367
FT DOMAIN 368 374
FT TRANSSEM 375 399
FT DOMAIN 400 562
FT CARBOHYD 60 60
FT CARBOHYD 76 76
FT LIPID 413 413
FT DOMAIN 21 57
FT DOMAIN 416 421
FT CONFLICT 330 330
SQ SEQUENCE 562 AA; 59857 MW; 6CF151B5F7FA47 CRC64;

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Query Match 12.0%; Score 317.5; DB 1; Length 562;  
 Best local similarity 23.3%; Pred. No. 2e-11;  
 Matches 103; Conservative 60; Mismatches 161; Indels 119; Gaps 10;

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QY 29 AHGIRSVLVYFLAASVGNIVLALVQKRPOLQVNTNRTFNLVTDLIQISLVAPVW 88
DB 88 AAGVGVGVEFLAFLITTAAGNMLVLLSVACNRHQLQTVNYPVIMVAADLLSAVLPFS 147
QY 89 VATSVPLFPLNSHFCALVSLTHLFAFASVNTIVLSVDKYLSTIHPISPKMTORBG 148
DB 148 ATMEVLGWPGRPTCDVMAVDVLCASLISCTISVDYGVGRHSKTPAINTERKA 207
QY 149 YLLYGTVIAVILLOSTPPLYGWQ-AAFDERNALCSMTIGASPSYTLISVSVFTIPLIV 207
DB 208 AAILALMAVALVSVGLLGMKEVPEDER--FCGIT--EYGVATFPSSVCSFYLPMAV 263
QY 208 MIACYSVFCAARROHALLVVKRHSLEVRYKDCVENDEDEGAKKEFEODESEFRQHE 267
DB 264 IVVMICRYVVAR-----TRSLKAGIK-----REP 290
QY 268 GEVAKKEGRMEAKDGLKAKEGSTGTSSEVSEARGESEVRSTVSDSGMEKGSTKY 327
DB 291 GKASEVILRIHRCRAAISAK-GNPGTOS----- 318
QY 328 EENSMKADKRGTEVNOCSIDLGEDMEFGEEDDINFSEDDVEAVNIPESLPPSRNNSNP 387
DB 319 -----KGTILNLSLVRL-----LAFSRK----- 338
QY 388 PLPRCYOCKAAKVFIFIIFSVLSLGPYCLAVLAWVDVETQVQWITITIIWFLQCC 447
DB 339 -----KAKTLAIYGVGVFLCMFPFFVPLGS-LFPOLKPSCEGVFKVIFWLYGFNS 389
QY 448 CIHPYVYGMHTIKKEIQDMLK 470
DB 390 CVNPILPCSSREKRAFLRLR 412

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Search completed: October 28, 2002, 16:45:59  
 Job time : 17 secs

DE 5-hydroxytryptamine receptor (5-HT receptor) (Serotonin receptor).  
OS *Lymanaea stagnalis* (great pond snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC *Lymaneidae*; *Lymanaea*.  
OX NCBI\_Taxid=6523;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93126323; PubMed=809356;  
RA Sugamori K.S., Sunahara R.K., Guan H.-C., Bulloch A.G., Tensen C.P.,  
RA Seeman P., Niznik H.B., van Tol H.H.;  
RT "Serotonin receptor cDNA cloned from *Lymanaea stagnalis*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:11-15(1993).  
CC -!- FUNCTION: THIS IS A RECEPTOR FOR 5-HYDROXYTRYPTAMINE (SEROTONIN),  
CC A BIOGENIC HORMONE THAT FUNCTION AS A NEUROTRANSMITTER, A HORMONE,  
CC AND A MITOGEN.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
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CC -----  
DR EMBL; L06803; AAA29290.1; -.  
DR GCRDB; GCR\_0520; -.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1.1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; G-PROTEIN\_RECPT\_FL\_1; 1.  
DR PROSITE; PS50262; G-PROTEIN\_RECPT\_FL\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
FT DOMAIN 1 99  
FT TRANSMEM 100 122  
FT DOMAIN 123 132  
FT TRANSMEM 133 154  
FT DOMAIN 155 169  
FT TRANSMEM 170 191  
FT DOMAIN 192 210  
FT TRANSMEM 211 233  
FT DOMAIN 234 259  
FT TRANSMEM 260 281  
FT DOMAIN 282 432  
FT TRANSMEM 433 456  
FT DOMAIN 457 465  
FT TRANSMEM 466 488  
FT DOMAIN 489 509  
FT CARBOHYD 3 3  
FT CARBOHYD 47 47  
FT CARBOHYD 58 58  
FT CARBOHYD 68 68  
FT CARBOHYD 72 72  
FT CARBOHYD 78 78  
FT DISULFID 168 246  
SQ SEQUENCE 509 AA; 56902 MW; D283696C8C50B18 CMC64;  
Query Match 12.1%; Score 319; DB 1; Length 509;  
Best Local Similarity 22.3%; Pred. No. 1,56-11;  
Matches 108; Conservative 96; Mismatches 205; Indels 76; Gaps 14;  
QY 3 STCNSTPSSSSHHCMPLSKMPTSLAGIIRSYLYVELFAASFGN--IYIALVLOKKP 60  
Db 74 TSSATNMDDRWLSLTV-----YSHEHLVLTYSVLGLFVLCCTIGNCFVIAAWLER-- 124  
QY 61 QLDQVTRNFELNLTVDLQISLVAPVVAATVPELPLNSHFCATSLTHLFAFASVN 120  
Db 125 SLHVVAVNLILSLAVADLMVAVLVWPLSVSEISKVMPLSHBEVCDMTSLVDVLCCTASIL 184  
QY 121 TIVLVSDRYSLIHPILSPSKMTQRRKYLILGLGVIYALIIQSTPPLPGKCAAFD-ERN 179  
Db 185 HLVAIDRRYAAVY-SDIYIRRSRSLRLIMVMVYIAFLFSLTSPPLGWRPNNDPKT 243

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RT      "Molecular cloning and expression of the cDNA for a novel alpha 1-
RT      adrenergic receptor subtype."
RL      J. Biol. Chem. 265:8183-8189(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92087349; PubMed=1966743;
RA      Schwinn D.A., Coccechia S., Lorenz W., Caron M.G., Lefkowitz R.J.;
RT      "The alpha 1C-adrenergic receptor: a new member in the alpha 1-
RT      adrenergic receptor family";
RL      Trans. Assoc. Am. Physicians 103:112-118(1990).
CC      -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC      ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC      CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(O)
CC      AND G(11) PROTEINS.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL: J05426; AAA30374.1; -.
DR      PIR: A35375; A35375.
DR      GCRDB: GCR_0004; -.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.
DR      PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR      PROSITE: PS50262; G-PROTEIN RECEPTOR FL 2; 1.
KM      G-protein coupled receptor; transmembrane; glycoprotein;
KM      Multigene family; phosphorylation; lipoprotein; palmitate.
FT      DOMAIN 1 27
FT      TRANSSEM 28 51
FT      DOMAIN 52 64
FT      TRANSSEM 65 88
FT      DOMAIN 89 99
FT      TRANSSEM 100 122
FT      DOMAIN 123 143
FT      TRANSSEM 144 167
FT      DOMAIN 168 181
FT      TRANSSEM 182 205
FT      DOMAIN 206 273
FT      TRANSSEM 274 297
FT      DOMAIN 298 305
FT      TRANSSEM 306 329
FT      DOMAIN 330 466
FT      CARBOHYD 7
FT      CARBOHYD 13
FT      CARBOHYD 22
FT      MOD_RES 215
FT      DISULFID 99
FT      LIPID 345
FT      SEQUENCE 466 AA; 51466 MW; 77635153B39E85EC CRC64;

Query Match 12.3%; Score 325.5; DB 1; Length 466;
Best Local Similarity 20.4%; Pred. No. 5.7e-12;
Matches 107; Conservative 78; Mismatches 182; Indels 157; Gaps 10;

OY      7 NSTRESSSHHCMPKSPISLANHGIIRSVLVFLAASFGVGNVLAIVLQRPQLOVLT 66
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      7 NASDSNCTH-----PPPPVNISSKAILLGVILGILFVGNILVILSVACHRLHSVT 61
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      67 NRIFFNLVTDLQISLVAPWVATSVLPFNPNSHCTALVSLTHLFAFASVNTIVLV 126
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      62 HYIVVNAVALDLITLVLPESAIFELIGYWAFCVFCVWMAADVLCCTASIMGLCIIS 121
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      127 VDRLSIITHPLSPYSKMTQGRGYLLLTGTWIVAIQSTPPPLYGMOQAQFDRNALCMIW 186
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

DB      122 IDRIYIGSVPLRYKPTIVIQKRGIMALLCWMALSLVISTIGPLFGMRQA-PEDETICQI-- 178
OY      187 GASPSYITLISVSPFIVPLIYWIACYSVFCARQOHALLIVNKRHSLEVRKDCVENED 246
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      179 NEEPGYVLFSAIGSPYVPLITLIVMCRVYVAKR----- 213
OY      247 EGCARKKEEPQDESEFRROHESEVYAKGSRMAKNGKSLAKKEGSGTSESSVEANGSREV 306
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      214 -----ESRG----- 217
OY      307 RESSTVADSGMEKSGTKVEENSMKADGTEVNOCSIDGEDMEFGEDDINFSDD 366
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      218 -----LKSGLTKDSDS---EQVTLRIHRKNAQVGGSGVNSAKKTFVRLKFSREK 268
OY      367 VEAVNIPESLPSSRRNSNPPLPRCYOCCAKAKVIFITFISVLSGPFCLAVLAWVD 426
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      269 -----KAKTGIYVGFVLCWLPF-FLVWPIGSFF 298
OY      427 VETQVPQWVITITLWFLQCCIHPYVGYMHTIKKEIOMLKKEFPCKEPRK----- 480
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      299 PDERSEVFKIAPWLGVLNSCINPIIYPCSSQEFKAPQWVRLIQCLRRQSSKHTLGY 358
OY      481 -----EDSHPDL-----PTEGSGTEGKIVPS 501
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
OY      359 TLHAPSHVLEQHKDLVRIPIVGSATFYKISKTDGVCMEKIFSS 402
OY      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:

RESULT 13
5H1B_FUGRU STANDARD: PRT; 416 AA.
AC 042384;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 5-hydroxytryptamine 1A-beta receptor (5-HT-1A-beta) (Serotonin
DE receptor) (5-HT1A-beta) (F1B).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97361762; PubMed=9218723;
RA Yamaguchi F., Brenner S.;
RT "Molecular cloning of 5-hydroxytryptamine (5-HT) type 1 receptor
RT genes from the Japanese puffer fish, Fugu rubripes.";
RL Gene 191:219-223(1997)
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC CYCLASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC STROMEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
-----
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CC      or send an email to license@isb-sib.ch).
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DR      EMBL: X95937; CA65176.1; -.
DR      HSSP: P02699; 1F88.
DR      GCRDB: GCR_2428; -.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.

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Db 299 PNEFPPEVTKIVFWLGYLNSCLNPIIYPCSSQEFKFAFONVLRIOCLRROSSKHALGY 358
OY 484 --HPDLPGTEGGTEGKI-VPSYDSATF 507
Db 359 TLHPPSOAVEQHRGMVIRPVGSETF 385

RESULT 11
SH1A-RAT STANDARD; PRT; 422 AA.
ID SH1A-RAT
AC P19327;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor) (5-HT1A).
GN HTR1A OR 5HT1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NC MBL_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90202832; Pubmed=2156831;
RA "Albert P.R., Zhou Q.-Y., Van Tol H.H.M., Bunzow J.R., Civelli O.;
RT "Cloning, functional expression, and mRNA tissue distribution of the
RT rat 5-hydroxytryptamine 1A receptor gene";
RL J. Biol. Chem. 265:5825-5832(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90355775; Pubmed=2167416;
RA Fujimura Y., Nelson D.L., Kashiwara K., Varga E., Roeske W.R.,
RT "Role of cytochrome P450 in the control of the production of
RT erythropoietin.";
RL Life Sci. 47:127-132(1990).
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC CYCLASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC SPONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
CC -----
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CC -----
DR EMBL; J05276; AAA40612.1; -.
DR PIR; A35181; A35181.
DR PIR; JH0315; JH0315.
DR HSP; P29274; 1MHM.
DR GCRDB; GCR_0109; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 37 62 1 (POTENTIAL).
FT DOMAIN 63 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 98 2 (POTENTIAL).
FT DOMAIN 99 109 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 110 132 3 (POTENTIAL).
FT DOMAIN 133 152 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 153 178 4 (POTENTIAL).
FT DOMAIN 179 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 217 5 (POTENTIAL).
FT DOMAIN 218 345 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 346 367 6 (POTENTIAL).
FT DOMAIN 368 378 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 379 403 7 (POTENTIAL).
FT DOMAIN 404 422 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 109 187 BY SIMILARITY.
FT CONFLICT 373 373 S -> N (IN REF. 2).
SQ SEQUENCE 422 AA; 46429 MW; 19C2731834C4BC9 CRC64;

Query Match 12.6%; Score 332.5; DB 1; Length 422;
Best Local Similarity 23.5%; Pred. No. 2.1e-12;
Matches 111; Conservative 76; Mismatches 181; Indels 105; Gaps 12;

OY 26 ISLHGIRSTVLYIFLAASFVN--IYALVLGRKPOLGVNRFNFIPLVTLQLQISL 83
Db 31 VTFSYQVITSLTLGLIFCAVLGNACVVAIALER--SLQNVANYLIGSLAVTDLMSVL 88
OY 84 VAPWVATVPLEFPLNSHCTALVSLTHLPAFASVNTIVLVSDRYLSIHPDPSKM 143
Db 89 VLPMAALYQVLNKKWTLGGVTCDFLADLVLCSTSIHLCAIALDRYWAITDPIDYVKR 148
OY 144 TORRGYLLYTWIVAILQSTPRPLXGQGAFFDERNALCSIMKASPSYTLISVVSFVI 203
Db 149 TPRRAALISLTWLIIGFLISIPMLGMWTP--EKSDDPACTIKDHQYITSTFGAFYI 206
OY 204 PLIVAIACYSVFPCARFOHALVNVKHSLEVRKQDVEENDEGAERKEEFODESEFR 263
Db 207 PLLMLVLYGKIFRARR-----FRIRKIVRVEKKGA----- 238
OY 264 ROHEGEYNAKGRMEADKSLKANEGSTGTSESSVEARSGSEVRBSSTVASDGSMEGEG 323
Db 239 -----GTS-----LTSSAPPPKKSLNGQPG 259
OY 324 S--TKVENSMKADKGTENVQCSIDGEDMERGEDINFSDDVAV--NIDESLP-P 378
Db 260 SGDMWRCAEN-----RAVGTPCT--NGAVRGDDEATLEVIRVANSKEHPLP 308
OY 379 SRNNSNMP-----LPRCYQCAAKVYFIIFSIVSLGPGFLAVLA 422
Db 309 SESSGNSYAPACLEKRNERNNAEKRMALAREKTVKLGIMGFILCWLPFIYALVL 368
OY 423 VWVDVETVPQWVITIIIMLFLOCCHIPVYGYVHKTIKEIDMKPFCK 475
Db 369 PECESSCHMPALGAIINWLGYSNLSINPVIYAVFNKDFQNAFKIKCKPCR 421

RESULT 12
A1AA_BOVIN STANDARD; PRT; 466 AA.
ID A1AA_BOVIN
AC P18130;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE Alpha-1A adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90243698; Pubmed=1970822;
RA Schwinn D.A., Lomasney J.W., Lorenz W., Szklut P.J., Fremeanu R.T., Jr.,
RA Yang-Feng T.L., Caron M.G., Leikowitz R.J., Cotecchia S.;

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Db 42 LSYQIITSLFGLALILCSIFGNSCVAAIALER--SLQNVANYLIGSLAVTDLNVSVLV 99
QY 86 PMWVATSVPLFMPNLSHPTALVSLTHLFAFASVNTIVSVDRYLSLTHPLVSFPMQ 145
Db 100 PMALVLYLKKWTLGODICDLFDLVCCCTSSILHICAILDRYMAITPDIYVNRTP 159
QY 146 RRGVLLYGTIVAVILLOSTPPLVGMGOAFDERNALCSMWGASPSYTLISVVFYIPL 205
Db 160 RRAAVLSVWMLIGFSITPMLGM-RAEDBRAPDACCII-SQDPGTIVTSPCAFYIPL 217
QY 206 IVMVACTSVVFCARRRHALLYNKRHSLEYRKDCVENDESGAEKKEEFQDESERRQ 265
Db 218 ILMVLVLRGIFPKAR-----FRIKRTVKKTEKAKASVMCLTILSPAVFHKR 262
QY 266 HEGEVKAKESGMEKDGSLAKESGTSSTSSVARGSESEVRSTVASDGSMDGKSGST 325
Db 263 ANGA-----VSAEMKRGYKFKPSPCANCAVRHGE-- 294
QY 326 KVEENSMKADKGRTEVNCSDIDGEDMERGEDDINFSEDDVEAVNIPESLPPSRNSNS 385
Db 295 -----MESLEIEVNSN-SKTHLPLPNTPOS--SSHENINE 327
QY 386 NPLPLP-----CYOCKAKAVYIIIFSYVLSLGPYCLAVLAVVDVETQVQAVITII 440
Db 328 KTGTEFRKIALARERKTVKTLGIMGTIFCWLPEFTVALVLPFCAENCYMPFWLGAVIN 387
QY 441 WLFLOCCIHPRYYGVYGMHKTITKKEIOMLKKFPCK 475
Db 388 WLGYSNLSLNPITVYAFNKPDSAFKKILR--CK 419

RESULT 10
ALIA_MOUSE STANDARD; PRT; 466 AA.
ID P97718; 054913;
DT 15-JUL-1998 (Rel. 36, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-1a adrenergic receptor (Alpha 1a-adrenoceptor) (Alpha-1C
  adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RC STRAIN=CD-1; TISSUE=Brain, and Kidney;
RX MEDLINE=98292316; Pubmed=9630362;
RA Xiao L., Scofield M.A., Jeffries W.B.;
RT "Molecular cloning, expression and characterization of cDNA encoding a
  mouse alpha1a-adrenoceptor."
RL Br. J. Pharmacol. 124:213-221(1998).
RN [2]
RP SEQUENCE OF 197-280 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96064818; Pubmed=7595531;
RA Alonso-Llamazares A., Zamanillo D., Casanova E., Ovalle S., Calvo P.,
  Chinchetru M.A.;
RT "Molecular cloning of alpha 1d-adrenergic receptor and tissue
  distribution of three alpha 1d-adrenergic receptor subtypes in
  mouse."
RL J. Neurochem. 65:2387-2392(1995).
CC - FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
  ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
  CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(O)
  AND G(11) PROTEINS.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED
  (BY SIMILARITY).
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: AF031431; AAC02658.1; -.
DR EMBL: S80220; AAB47044.1; ALT_INIT.
DR MGD: MGI:104773; Aqrata.
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 27
  EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 28 51
  1 (POTENTIAL).
FT DOMAIN 52 64
  CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 65 88
  2 (POTENTIAL).
FT DOMAIN 89 99
  EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 100 122
  3 (POTENTIAL).
FT DOMAIN 123 143
  CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 144 167
  4 (POTENTIAL).
FT DOMAIN 168 181
  EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 182 205
  5 (POTENTIAL).
FT DOMAIN 206 273
  CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 274 297
  6 (POTENTIAL).
FT DOMAIN 298 305
  EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 306 329
  7 (POTENTIAL).
FT DOMAIN 330 466
  CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7
  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 13 13
  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 22 22
  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 215 215
  PHOSPHORYLATION (BY CARK) (POTENTIAL).
FT LIPID 99 176
  BY SIMILARITY.
FT LIPID 345 345
  PALMITATE (POTENTIAL).
FT SEQUENCE 466 AA; 51762 MW; 36495A53DBD34DA CRC64;

Query Match 12.6%; Score 333; DB 1; Length 466;
Best Local Similarity 22.5%; Pred. No. 2,1e-12;
Matches 114; Conservative 75; Mismatches 184; Indels 134; Gaps 13;

QY 7 NSTRENSHTCMPLSKMPISLAGIIRSYLVIFPLASFNGINVLVLOKQOLLOYT 66
Db 7 NASGSGNCTH---PPAONISKA--ILGVLIGGLIFGVGNLIVLIVSACHRHLSVT 61
QY 67 NRETFNLVTDLDLSIVAPWVATSVPLFMPNLSHPTALVSLTHLFAFASVNTIVLV 126
Db 62 HYIVNLAVALDLTLSTYLPFSAIFELIGVAFGRVFCNITMAADVLCCTASIMGCTIS 121
QY 127 VDRYLSIHLPLSPSKMTQRGYLLYGTWITVAILOSTPPLVGMGOAFDERNALCSMW 186
Db 122 IDRYIGVSYPLRPYPTIVQGRGVALLCVMALSVISIGPLFGWMOQA-PEDETICQ-- 178
QY 187 GASPSYTLISVSVFTVPLIYMIACYSVFCARRRHALLYNKRHSLEYRKDCVENED 246
Db 179 NEEPGYVLFSAIGSRYPVLTJILWYCRVYVARK-----BSRG 217
QY 247 EGAEKKEEFQDESEFRHGEVAKGRMEADGSLAKESGTSSTSSVARGSESEVR 306
Db 218 LKSGIKTDKSDSEOVTLRIHKRWPA-----EGS-GYSSA----- 251
QY 307 RESSTVASDGSMEKESGTSKVEENSMKADKGRTEVNCSDIDGEDMERGEDDINF 366
Db 252 -----KNKT-----HFSVRLKFSREK 268
QY 367 VEAVNIPESLPPSRNSNSNPLPRCYOCKAKAVYIIIFSYVLSLGPYCLAVLAVWD 426
Db 269 -----KAAKTLGIYVGVFCVLCWLPF-FLVWVIGSFF 298
QY 427 VETQVQWVITIIITWLFLOCCIHPRYYGVYGMHKTITKKEIOMLKKFPCKEAPKEDS--- 483
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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multigene family.
FT DOMAIN 1 36
FT TRANSMEM 37 62
FT DOMAIN 63 73
FT TRANSMEM 74 98
FT DOMAIN 99 109
FT TRANSMEM 110 132
FT DOMAIN 133 152
FT TRANSMEM 153 178
FT DOMAIN 179 191
FT TRANSMEM 192 217
FT DOMAIN 218 345
FT TRANSMEM 346 367
FT DOMAIN 368 378
FT TRANSMEM 379 403
FT DOMAIN 404 421
FT CARBOHYD 10 10
FT CARBOHYD 11 11
FT CARBOHYD 24 24
FT CARBOHYD 30 30
FT DISULFID 109 187
FT VARIANT 17 19
FT CONFLICT 177 177
FT CONFLICT 242 242
FT CONFLICT 247 247
FT CONFLICT 263 263
FT CONFLICT 304 304
SQ SEQUENCE 421 AA; 46123 MW; CD8519D37A1F499B CRC64;

Query Match 12.7%; Score 335.5; DB 1; Length 421;
Best Local Similarity 23.2%; Pred. No. 1,4e-12;
Matches 106; Conservative 88; Mismatches 190; Indels 73; Gaps 12;

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AC 042385;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 5-hydroxytryptamine 1A-alpha receptor (5-HT-1A-alpha) (Serotonin
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97361762; PubMed=9218723;
RA Yamaguchi F., Brenner S.;
RT "Molecular cloning of 5-hydroxytryptamine (5-HT) type 1 receptor
genes from the Japanese puffer fish, Fugu rubripes.";
RL Gene 191:219-223(1997).
CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYLATE
CYCLASE ACTIVITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
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or send an email to license@isb-sib.ch).
CC
DR EMBL; X95936; CAA65175.1; -.
DR GDB; GCR 2429; -.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multigene family.
FT DOMAIN 1 45
FT TRANSMEM 46 71
FT DOMAIN 72 82
FT TRANSMEM 83 107
FT DOMAIN 108 118
FT TRANSMEM 119 141
FT DOMAIN 142 161
FT TRANSMEM 162 186
FT DOMAIN 188 200
FT TRANSMEM 201 226
FT DOMAIN 227 346
FT TRANSMEM 347 368
FT DOMAIN 369 379
FT TRANSMEM 380 404
FT DOMAIN 405 423
FT CARBOHYD 118 196
FT DISULFID 9 9
FT CARBOHYD 12 12
FT CARBOHYD 30 30
SQ SEQUENCE 423 AA; 47000 MW; 7B1308626B40190F CRC64;

Query Match 12.6%; Score 333; DB 1; Length 423;
Best Local Similarity 24.0%; Pred. No. 1,9e-12;
Matches 109; Conservative 74; Mismatches 188; Indels 84; Gaps 11;

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RC TISSUE-Prostate; PubMed=8396931;  
 RX MEDLINE=93384619;  
 RA Hirasawa A., Horie K., Tanaka T., Takagaki K., Mural M., Yano J.,  
 RA Tsujimoto G.,  
 RT "Cloning, functional expression and tissue distribution of human cDNA  
 RT for the alpha 1C-adrenergic receptor.";  
 RL Biochem. Biophys. Res. Commun. 195;902-909(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Tseng-Crank J.C., Goetz A., Saussy D., Robertson K.M., Hazum S.,  
 RA Hatzilip J., Godinot N., Wisely B., Robertson C.N., Kost T.,  
 RL Submitted (Oct-1993) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Lymphocytes; and Hippocampus;  
 RX MEDLINE=94239386; PubMed=8183249;  
 RA Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang R.,  
 RA Lepor H., Hartig P.R., Weinschenk R.L., Branchek T.A.,  
 RA Gluchowski C.,  
 RA "The alpha 1-adrenergic receptor that mediates smooth muscle  
 RT contraction in human prostate has the pharmacological properties of  
 RT the cloned human alpha 1C subtype.";  
 RL Mol. Pharmacol. 45;703-708(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95114877; PubMed=7815325;  
 RA Schain D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,  
 RA Worman N.P., Campbell S., Fidock M.D., Furness L.M.,  
 RA Parry-Smith D.J., Peter B., Bailey D.S.,  
 RT "Cloning and pharmacological characterization of human alpha-1  
 RT adrenergic receptors: sequence corrections and direct comparison with  
 RT other species homologues.";  
 RL J. Pharmacol. Exp. Ther. 272;134-142(1995).  
 CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY  
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-  
 CC CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)  
 CC AND G(11) PROTEINS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: HEART, BRAIN, LIVER AND PROSTATE, BUT NOT IN  
 CC KIDNEY, LUNG, ADRENAL, AORTA AND PITUITARY.  
 CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED  
 CC (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D25235; BAA0960.1; -  
 CC EMBL: U02569; AAA93114.1; -  
 CC EMBL: U03866; AAB60353.1; -  
 CC EMBL: L31774; AAB59486.1; -  
 CC GCRD: GCR\_0542; -  
 CC GCRD: GCR\_0802; -  
 CC GCRD: GCR\_1016; -  
 CC GCRD: GCR\_1881; -  
 CC MIM: L04221; -  
 CC InterPro: IPR000276; GPCR\_Rhodopsin.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR00237; GPCR\_RHODOPSIN.  
 CC PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 CC PROSITE: PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
 CC Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 28 31 1 (POTENTIAL).  
 FT TRANSSEM 52 64 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 65 88 2 (POTENTIAL).  
 FT DOMAIN 89 99 EXTRACELLULAR (POTENTIAL).

FT	TRANSSEM	100	122	3 (POTENTIAL).
FT	DOMAIN	123	143	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	148	167	4 (POTENTIAL).
FT	DOMAIN	168	181	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	182	205	5 (POTENTIAL).
FT	DOMAIN	206	273	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	274	297	6 (POTENTIAL).
FT	DOMAIN	298	305	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	306	329	7 (POTENTIAL).
FT	DOMAIN	330	466	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	7	7	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	13	13	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	22	22	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD. RES	215	215	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	DISULFID	99	176	BY SIMILARITY.
FT	LIPID	345	345	PALMITATE (POTENTIAL).
FT	CONFLICT	43	43	G -> C (IN REF. 2).
FT	CONFLICT	129	129	S -> T (IN REF. 2).
FT	CONFLICT	347	347	C -> R (IN REF. 1 AND 4).
FT	CONFLICT	359	359	T -> P (IN REF. 2).
FT	CONFLICT	431	431	O -> E (IN REF. 1).
FT	CONFLICT	442	442	S -> C (IN REF. 2).
FT	CONFLICT	442	442	S -> C (IN REF. 2).
FT	SEQUENCE	466 AA;	51486 MW;	1A50487531DECDFO CRC64;

Query Match 12.8%; Score 338.5; DB 1; Length 466;  
 Best Local Similarity 21.3%; Pred. No. 1e-12;  
 Matches 108; Conservativity 80; Mismatches 187; Indels 131; Gaps 11;

QY	8	STRESSNSHTCMPLSKMPISLANGITRSYVLFYFLAEPVGNVNLVLRKQQLQVYN	67
DB	5	SCNADSSNCTOP--PAPVMSKAILLGVLLGGLVGNLVLILSVACHRHLSVTH	62
QY	68	REFINLLYDLQISVAPVNVATSVPLPMSHFCETALVSLTHFAFASVNTIYLVSY	127
DB	63	YVYNVAVNALDLTSTVLPVLSAIFELVGVAFGRVNCNMAADVLCSTASINGLQISL	122
QY	128	DRYLSIHLPLSPSKTORRGVLLYGTWVAILQSTPPLVYGQAADFERNALCSNWK	187
DB	123	DRYGVSYPLRPLTYVQRGLMALCYMALSLVLSIGPLFGWOPA-PEDETICOT--N	179
QY	188	ASPSYTLISVSVFLVPLIYMIACYSVPCARQNALLVNVRHSLLEVAVKOCVEDE	247
DB	180	EEPPYVLFSAIGSFYPLALILVWYCRVYVAK--	218
QY	248	EGAEKKEFODESEFRQHGEEVAKEGMEAKDGLAKEGSTGSESSVEARGSEVR	307
DB	219	KSGIKTKSKSEQVYTLAIHKKNVA-----GGSGMASAKTKTHFSVRL-	261
QY	308	ESSTVASDGSMEKGEKSTKYBENSMAKDKGRTVEVNOCSIDLGEDMFGEDDI	367
DB	262	-----LKSREK- 268	
QY	368	EAVNIPESLPPSRNSNSNPPLPRCYOCKAKAVFIILFSYLSLGYCFVLAVVWDV	427
DB	269	-----KAATLGIYVCGVLCWLPF-FLVMPTGSGFP 299	
QY	428	ETQVPQWVITITIMFLFLOCCIHRYVGYMHTIKKEIDMKL-KFCKECPPE----	482
DB	300	DKRSEYFKIVFWLGYLNCINPLIYPCSSQERKKAQVNLRIQCRCRQSKHALGYT	359
QY	483	SHPLPGTEGTECKI-VPSTDSATF 507	
DB	360	LHPSQAVEGQHKDMVRIPVGSRETF 385	

RESULT 6  
 ID A1AA\_CAVPO STANDARD; PRT: 466 AA.  
 AC 09WU25;  
 DC 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C

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Db 122 IDRIQSVYPLRPTIYVORGRRLALLCVAFSLVSVGLFPGMRPADPD-ETICQI-- 178
QY 187 GASPSYILSVSEFIYIPLVIMTACYSVFCARROHALLYNKRHSLEVRKDCVENED 246
Db 179 NEEPGYLSALDSFYVPLTIITIAMCRVYVAKR-----ESRG 217
QY 247 EEGAEEKEEPQDESEFRROHEGEVAKEGMEAKDGLAKEGSTGTSTSESSVEARGSEEV 306
Db 218 LKSGLTAKDSQVTLRIHRKNAP-----GGSGVASA----- 251
QY 307 RESSTVASDGSMEGKEGSTVENSMAKADGRTEVNOCSIDLGEDMFEDEEDINSEDD 366
Db 252 -----KNKT-----HFSVRLKFSREK 268
QY 367 VEAVNIPESLPSPRRNSNPPLPRCYCKAAVYFIIFSVYLSGPGCEFLAVLAWVD 426
Db 269 -----KAKTLGIVGCEFLCWLPLF-FLVWPIGTSFF 298
QY 427 VETQVQWVITIIWLFEFLQCCIHPPVYGYMHKTIKKEIDMK 470
Db 299 PDEKPEVYKIVEMVLGYLNSCINPIYPCSSQEFKKAQNVLK 342

RESULT 4
A1AA_ORYLA
ID A1AA_ORYLA STANDARD; PRT; 470 AA.
AC 091175;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alpha-1A adrenergic receptor (MARL).
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
  Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
  Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96184522; PubMed=8654394;
  Yasuoka A., Abe K., Arai S., Emori Y.;
  "Molecular cloning and functional expression of the
  alpha1A-adrenoceptor of Medaka fish, Oryzias latipes.";
  Eur. J. Biochem. 235:501-507(1996).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
  ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
  CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D63859; BAA09921.1; -
DR GCRD: GCR_1567; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 51 1 (POTENTIAL).
FT DOMAIN 52 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 88 2 (POTENTIAL).
FT DOMAIN 89 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 122 3 (POTENTIAL).
RP

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FT DOMAIN 123 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 167 4 (POTENTIAL).
FT DOMAIN 168 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 205 5 (POTENTIAL).
FT DOMAIN 206 221 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 272 295 6 (POTENTIAL).
FT DOMAIN 296 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 327 7 (POTENTIAL).
FT DOMAIN 328 470 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 12 12 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 99 176 BY SIMILARITY.
FT LIPID 343 343 PALMITATE (POTENTIAL).
FT DOMAIN 351 354 POLY-HIS.
SQ SEQUENCE 470 AA; 51925 MW; D4F7A8303061D4E CRC64;

Query Match 12.98; Score 340; DB 1; Length 470;
Best Local Similarity 23.88; Pred. No. 8,6e-13;
Matches 119; Conservative 66; Mismatches 180; Indels 134; Gaps 14;

QY 12 SNSGHTCMPLSKMPSISLAHGIRSTVLVIFLAASFVNIVLALYQKRPOLLYQTNREIF 71
Db 11 SNCSHVLP-----ELNIVKAVLGMVLGIFILFEGVIGNILVILSVGRHLQTYTYFIV 66
QY 72 NLVTDLLQISLVAPWVAVTSVPLFMPLNSHFCTALVSLTHLFAFASVNTIVLVSVDRL 131
Db 67 NLAVADLLSTVLPSFAIFELDRWVGFRVCEIMAAVLDICTASIMSLCVISVDRI 126
QY 132 SIHPLSPSKMTORRGYLLGLGTWVAILIOSTPPLPGWGOAARDERNALCSMTWGS 191
Db 127 GVSYPLEKYPALMTKRRLALLMVLMLVLSIIGPLGKWEPA--PEDEYCKIT--EEPG 183
QY 192 YTLISVSEFIYIPLVIMTACYSVFCARROHALLYNKRHSLEVRKDCVENEDGAE 251
Db 184 YATSAVGSFTPLAITIITIAMCRVYVAAQKSRK-----KKG-Q 222
QY 252 KKEEFODESEFRROHEGEVAKEGMEAKDGLAKEGSTGTSTSESSVEARGSEEVRESST 311
Db 223 KIEKSDSEQVILRMHRG-----NTT 242
QY 312 VASGSGMEGKEGSTVENSMAKADGRTEVNOCSIDLGEDMFEDEEDINSEDDVAVN 371
Db 243 VSED-----EALRSRT-----HRLRLKFSREK----- 266
QY 372 IPESLPSPRRNSNPPLPRCYCKAAVYFIIFSVYLSGPGCEFLAVLAWVDVEYQ 431
Db 267 -----KAKTLGIVGCEFLCWLPLF-FLVLPISIPAYR 300
QY 432 P-QWVITIIWLFEFLQCCIHPPVYGYMHKTIKKEIDMKKFFCKEPPKEDSHPDLPGT 490
Db 301 PSDVFPKITEFLGFGFNSCINPIIYILCSNQEKKAFQSL-LGVHCLRMTPRAHHH-HLSVG 358
QY 491 EGGTEG-KIVPSYDASATP 508
Db 359 OSOTQGHSLRTISDSKGP 377

RESULT 5
A1AA_HUMAN
ID A1AA_HUMAN STANDARD; PRT; 466 AA.
AC P35348;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
  adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eulhertia; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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FT TRANSMEM 379 403 7 (POTENTIAL).
FT DOMAIN 404 422 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 109 187 BY SIMILARITY.
FT VARIANT 16 16 P -> L.
FT VARIANT 22 22 /FTID-VAR_003446.
FT VARIANT 22 22 G -> S (IN DBSNP:1799920).
FT VARIANT 28 28 /FTID-VAR_011826.
FT VARIANT 184 184 I -> V (IN DBSNP:1799921).
FT VARIANT 184 184 P -> L (IN DBSNP:1800043).
FT VARIANT 220 220 /FTID-VAR_011828.
FT VARIANT 220 220 R -> L (IN DBSNP:1800044).
FT VARIANT 272 272 /FTID-VAR_011829.
FT VARIANT 273 273 G -> D.
FT VARIANT 273 273 G -> D (IN DBSNP:1800042).
FT CONFLICT 152 154 /FTID-VAR_011830.
FT CONFLICT 172 172 RAA -> PR (IN REF. 1).
FT CONFLICT 418 418 M -> I (IN REF. 1).
FT CONFLICT 418 418 K -> N (IN REF. 1).
SQ SEQUENCE 422 AA; 46106 MW; 762664FC62CFD8F CRC64;

Query Match 12.9%; Score 340.5; DB 1; Length 422;
Best Local Similarity 22.0%; Pred. No. 7.2e-13;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=97324192; PubMed=9180361;
RA Miyamoto S., Taniguchi T., Suzuki F., Takita M., Kosaka N., Negro E.,
RA Okuda T., Kosaka H., Mureta S., Nakamura S., Akagi Y., Oshita M.,
RA Watanabe Y., Muramatsu I.;
RT "Cloning, functional expression and tissue distribution of rabbit
alpha1a-adrenoceptor."
RL Life Sci. 60:2069-2074(1997).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(O)
CC AND G(11) PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LIVER, VAS DEFERENS, BRAIN, AND
CC AORTA, BUT NOT IN HEART.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U81982; AAB6134.1; -
DR GCRDP; GCR_1290; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1. 1.
DR PRINTS; PR00237; GPCR_RHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_P1_1.
DR PROSITE; PS00262; G-PROTEIN_RECEPTOR_P2_1.
DR G-protein coupled receptor; Transmembrane; glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 51 1 (POTENTIAL).
FT DOMAIN 52 63 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 64 89 2 (POTENTIAL).
FT DOMAIN 90 99 3 (POTENTIAL).
FT TRANSMEM 100 122 4 (POTENTIAL).
FT DOMAIN 123 143 5 (POTENTIAL).
FT TRANSMEM 144 168 6 (POTENTIAL).
FT DOMAIN 169 181 7 (POTENTIAL).
FT TRANSMEM 182 205 8 (POTENTIAL).
FT DOMAIN 206 272 9 (POTENTIAL).
FT TRANSMEM 273 297 10 (POTENTIAL).
FT DOMAIN 298 304 11 (POTENTIAL).
FT TRANSMEM 305 329 12 (POTENTIAL).
FT DOMAIN 330 345 13 (POTENTIAL).
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 466 AA; 51365 MW; 9446D356B50DCD80 CRC64;

Query Match 12.9%; Score 340; DB 1; Length 466;
Best Local Similarity 22.0%; Pred. No. 8.5e-13;
Matches 102; Conservative 73; Mismatches 161; Indels 128; Gaps 9;

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RESULT 3
ALAA_RABIT
ID ALAA_RABIT STANDARD; PRT; 466 AA.
AC 002824;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Oryctolagus cuniculus (Rabbit).

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FT DOMAIN 139 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 181 4 (POTENTIAL).
FT DOMAIN 182 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 226 5 (POTENTIAL).
FT DOMAIN 227 412 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 413 433 6 (POTENTIAL).
FT DOMAIN 434 447 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 448 467 7 (POTENTIAL).
FT DOMAIN 468 490 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 115 195 BY SIMILARITY.
SQ SEQUENCE 490 AA; 54937 MW; 2CDFB5FA7D2298E CRC64;

Query Match 13.08; Score 343.5; DB 1; Length 490;
Best Local Similarity 23.7%; Pred. No. 5.7e-13;
Matches 116; Conservative 94; Mismatches 176; Indels 103; Gaps 17;

36 TVLVIFLA-----ASFVGNIVLALVLRKPOLQVTRFENLVTDL-----QISL 83
39 TVEIVFAIVYTGSLSTLVVGNILVMSLKVNROLQVNNIFLSLACADLLIGVSMNL 98
84 VAPWVAVTSVPLEWPNLSHCTALVSLTHLFAFASVNTIVLVSDRYLSIIFPLSPSKM 143
99 YTVYIING-----VWPLGAVVODLMLADYVSNASVNNLLISFDREYCYKPLTPARR 154
144 TORGYLLXGTWVALVLOSPPLYGW-----GQAFDERNALCSMIGASSTYIILSVS 199
155 TTKMAGLMAAAMWLSFLTLPALFLWQFVIGKRTVHERE--CYIOPLSNPAVTFGTAA 212
200 FIVPLVIMVACYSVFCARQHALLYNKRHSLEVR-----VKDCVEN 244
213 AFYIPVIMVLYLHILASGR-----VRRHKPESRKKRKKSLSPFRAPPKQNNNN 266
245 EDEGAKKEKKEPDESEFRROHEGEVAKKGRMEAKDGLAKEGSTGSSSEVARGSE 304
267 SPKRAVVEKEVRN-----GKV-----DDQPSAQTEANGQOEE-----KE 301
305 EVRESSVAVSGSMEKGEKSTKVEENSMKADKRTVENQCIDGEGDMEGEDDINPSE 364
302 TSNSSTSVSMQTQTKDP--TEELLPAQOGSPAHPRVNPYS-----KWSKIKIYTKQ 352
365 DDVEAVNIPESLP-----PSRRN--SNSNP--LPRCY-----OCKAAKV 400
353 TGTESVATIEIVPAKAGASDHNSLSNRPAVNAKPFASIASQYRKRRQMAARKKVTRT 412
401 IPIIFSVVLSLGYCEFLAVLVWVDVETQVQWVITIIWLFELQCCIHBYVYGYMHKT 460
413 IFAILLAFLITWTFYNNVVLINTE--CETCVPTVWSIGVLYCYNSTINPACVLCNAT 470
461 IKKEIOML 469
471 FKRTFKHL 479

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RX MEDLINE=87315369; PubMed=3041227;
RA Koblika B.K., Friele T., Collins S., Yang-Feng T.L., Kobilka T.S.,
RA Franke U., Lefkowitz R.J., Caron M.G.;
RT "An intronless gene encoding a potential member of the family of
RL receptors coupled to guanine nucleotide regulatory proteins."
RL Nature 329:75-79(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA Saltzman A.G., Morse B., Felder S.;
RL Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
RX FUNCTION
RP MEDLINE=8834700; PubMed=3138543;
RA Farqin A., Raymond J.R., Lohse M.L., Kobilka B.K., Caron M.G.,
RA Lefkowitz R.J.;
RT "The genomic clone G-21 which resembles a beta-adrenergic receptor
RL sequence encodes the 5-HT1A receptor."
RL Nature 335:358-360(1988).
RN [4]
RP VARIANT ASP-272.
RX MEDLINE=98425601; PubMed=9754630;
RA Kwanishi Y., Harada S., Tachikawa H., Okubo T., Shirashi H.;
RT "Novel mutations in the promoter and coding region of the human 5-HT1A
RL Am. J. Med. Genet. 81:434-439(1998).
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC CYCLASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
CC -----
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CC -----
DR EMBL; M28269; AAA36440.1; -
DR EMBL; X13556; CAA31908.1; -
DR EMBL; X57829; CAA40962.1; -
DR EMBL; M83181; AAA66493.1; -
DR PIR; S07343; S07343.
DR PIR; S31438; S31438.
DR HSSP; P29274; 1MH.
DR GCRDB; GCR_0087; -
DR GCRDB; GCR_0381; -
DR GCRDB; GCR_0624; -
DR MTM; 109760; -
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Polymorphism.
KM
FT DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 37 62 1 (POTENTIAL).
FT DOMAIN 63 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 98 2 (POTENTIAL).
FT DOMAIN 99 109 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 110 132 3 (POTENTIAL).
FT DOMAIN 133 152 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 153 178 4 (POTENTIAL).
FT DOMAIN 179 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 217 5 (POTENTIAL).
FT DOMAIN 218 345 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 346 367 6 (POTENTIAL).
FT DOMAIN 368 378 EXTRACELLULAR (POTENTIAL).

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OM protein - protein search, using sw model

Run on: October 28, 2002, 16:41:57 : Search time 14 Seconds  
(without alignments)  
1404.967 Million cell updates/sec

Title: US-09-992-238-2

Perfect score: 2644  
Sequence: 1 MSTCTNSTRESNSSHCTMP.....GTEGTEGKTIVPSYDSATFP 508

Scoring table: PHSUM62  
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343.5	13.0	490	1	ACMA_CHICK
2	340.5	12.9	422	1	SHIA_HUMAN
3	340	12.9	466	1	ALIA_RABIT
4	340	12.9	470	1	ALIA_ORYLA
5	338.5	12.8	466	1	ALIA_HUMAN
6	337.5	12.8	466	1	ALIA_CAVPO
7	336	12.7	466	1	ALIA_RAT
8	335.5	12.7	421	1	SHIA_MOUSE
9	333	12.6	423	1	SHIA_FUGRU
10	333	12.6	466	1	ALIA_MOUSE
11	332.5	12.6	422	1	SHIA_RAT
12	325.5	12.3	466	1	SHIA_BOVIN
13	320	12.1	416	1	SHIB_FUGRU
14	319	12.1	509	1	5HT_LYMSR
15	317.5	12.0	562	1	ALAD_MOUSE
16	314.5	11.9	572	1	ALAD_HUMAN
17	306.5	11.6	561	1	ALAD_RAT
18	304.5	11.5	484	1	ACMA_XENLA
19	304.5	11.5	484	1	OAR_DROME
20	300	11.3	576	1	ALAD_RABIT
21	292	11.0	479	1	ACMA_HUMAN
22	290	11.0	466	1	ACMA_RAT
23	288	10.9	295	1	ALIA_CANFA
24	288	10.9	488	1	YDWM_CABEL
25	287	10.9	466	1	ACMA_HUMAN
26	287	10.9	466	1	ACMA_MOUSE
27	283	10.7	515	1	ACMA_PIG
28	283	10.7	515	1	ALAB_MESAU
29	283	10.7	515	1	ALAB_RAT
30	283	10.7	519	1	ALAB_HUMAN
31	282	10.7	479	1	ACMA_MOUSE
32	281.5	10.6	478	1	ACMA_RAT
33	280	10.6	466	1	ACMA_CHICK

## ALIGNMENTS

RESULT 1	ID	ACMA_CHICK	STANDARD:	PRT:	490 AA.
AC	P17200	ACMA_CHICK			
DT	01-AUG-1990	(Rel. 15, Created)			
DT	01-AUG-1990	(Rel. 15, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Muscarinic acetylcholine receptor M4.				
CN	CHRM4.				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90153912; PubMed=2154460;				
RA	Tieffe K.M., Goldman P.S., Nathanson N.M.;				
RT	"Cloning and functional analysis of a gene encoding a novel				
RT	muscarinic acetylcholine receptor expressed in chick heart and				
RT	brain.";				
RT	J. Biol. Chem. 265:2828-2834(1990).				
CC	- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS				
CC	CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLYL CYCLASE,				
CC	BREAKDOWN OF PHOSPHOLIPIDS & MODULATION OF POTASSIUM CHANNELS				
CC	THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS				
CC	INHIBITION OF ADENYLYL CYCLASE. MAY COUPLE TO MULTIPLE FUNCTIONAL				
CC	RESPONSES IN CELL LINES.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN HEART AND BRAIN.				
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	EMBL: J05218; AAA48563.1; -				
DR	PIR: A35446; A35546.				
DR	CCRD: GCR 0010: -				
DR	InterPro: IPR000276; GPCR_Rhodopsn.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PRINTS: PR00237; GPCR_RHODOPSIN.				
DR	PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.				
DR	PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.				
KW	Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;				
KW	Phosphorylation; Multigene family; G-protein coupled receptor.				
FT	DOMAIN 1 42				
FT	TRANSSEM 43				
FT	DOMAIN 65 78				
FT	TRANSSEM 79 99				
FT	DOMAIN 100 116				
FT	TRANSSEM 117 138				

Q93126 balanus amp  
P08911 rattus norv  
Q25321 locusta mig  
P08912 homo sapien  
Q25322 locusta mig  
P14416 homo sapien  
P34969 bombyx mori  
Q17232 cavia porce  
P50407 drosophila  
P20905 meleagris g  
P52702 ceropithec

us-09-992-238-2.rpr

Page 9

Db 339 -----KAAKTLAIYGVFVLCWPEFFFLPLGS-LFPQLKPSGSEVFEVITFMILGYFNS 369

Qy 448 CIPHERYUYNMHTIKKEIQDMLK 470

Db 390 CVPPLIYCCSREKFRFLRLR 412

Search completed: October 28, 2002, 16:47:05  
Job time : 23 secs

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